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OM protein - protein search, using sw model

Run on:

March 29, 2003, 09:06:24; Search time 21.3633 Seconds (without alignments) 2141.995 Million cell updates/sec

US-09-758-173-12 2549 1 MKHLWFFLLLVAAPRWVLSQ......MHEALHNHYTQKSLSLSPGK 476 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 · 283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 2: pir2: \* 3: pir2: \* 4: pir4: \* PIR 73:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMMIN

	Description	chain	chain	chain	Ig gamma-2 chain C	chain	Ig heavy chain pre	chai	ď			ಹ	_	_	chain	U	Ig gamma 2b chain		Ig gamma 1 chain c		chain	cha	Ig heavy chain C r	heavy	υ	chain	chain	chain	cha	Ig gamma-3 chain C
SUMMARIES	ID	GHHU	A23511	A60764	G2HU	G4HU	\$22080	831459	869339	S37483	S40295	PC4436	S01321	G2MS11	147159	S31866	147160	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	PS0018	GIMS	G3MSC	GIMSM	G3MSM
	DB	-	7	N	Н	Н	7	~																				Н	Н	Н
	* Query Match Length	. "	377	377	326	327	470	472	374	469	446	444	475	474	328	255	328	234	328	323	328	329	308	289	326	333	324	329	393	398
	Query Match	69.2	ë.	c	62.8	a	-	0	60.7	56.0	4	54.2	3	53.4	•			49.0	48.1		48.0	47.6	•	45.2	45.0	•	•	44.6	44.4	44.2
	Score	17	626	1624.5	1600	1586.5	1567	1548	1547	1426.5	1392	1382.5	1369.5	1362	1259	1256	1253	1250	1227	1226.5	1223	1212.5	1157.5	1152	1148	1142.5	1138	1137	1133	1126
	Result No.		7	m	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

-	gamma-2a	gamma-2a	٠,	gamma-2	-	Ig gamma-2b chain	gamma 4 c	epsilon	Ig gamma-1 heavy c	Ig mu chain - shee	ьe	Ig Y heavy chain (	heavy	Ig heavy chain (DO	Ig mu chain precur
GZMSA	G2MSAB	G2MSAM	S00847	PS0019	806611	G2MSBM	147162	S38864	A49444	825705	S04845	B46529	S69340	869131	S14683
٦	-	Н	N	~	N	н	0	~	~	~	7	~	7	7	7
330	335	399	329	322	327	405	277	548	220	592	549	572	249	241	627
44.0	43.9	43.8	43.7	43.5	42.7	42.4	41.7	37.0	35.6	32.4	31.1	29.7	29.6	28.5	28.3
1122	1119.5	1117	1114.5	1108	1088.5	1080	1062	944	907	827	793.5	757.5	755.5	727.5	722
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

	ННО
	Ig gamma-1 chain C region - human
_	C; Species: Homo Bapiens (man)
	C.Date: 31-Jan 1981 #sequence revision 18-Aug-1982 #text Clange 16-041-1999 #
	A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
	A; Reference number: A93433; MUID: 82274238; PMID: 6287432
	A A CCERBIOL: ADJASS
	A;Residues: 1-330 <ell></ell>
-	L:Z17370
	A; Note: this sequence has the GIM(1) allotypic marker, 97-Lys, and the GIM(1) marker
	A;NOGE Lybe-34 IB removed arcer cranstacton B.Harria, T.J.
	submitted to the EMBL Data Library, October 1992
	A;Reference number: S33904
	A;Accession: S36861
	A;Molecule type: DNA
	A;Residues: 2-330 <har></har>
	A; Cross-references: EMBL: Z17370
	CELL 29, 0.1-0.7, 1982 N. mitl 29, 0.1-0.7 Human immunoclobulin gamma genes: implications for evolution of
	)
	A:Accession: S33887
	A: Wolecule type: DNA
_	A; Residues: 88-113; 235-330 <tak></tak>
	A;Cross-references: EMBL:Z17370
	R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
	Biochemistry 9, 3161-3170, 1970
	gammag-rimmingroburin: vii: Amtii acta
	Ajkelegelled immuet. Ayoloo, Nollo, teoroe, interpreta
_	A. Accession: Myconcapies and A. Accession: Myconcapies and My
	A; Molecule type: protein
	A;Residues: 1-96,'R',98-135 <cun></cun>
_	A, Note: this sequence has the Gim(3) marker, 97-Arg
	R;Ruttahauser, U.; Cunningham, B.A.; Bennert, C.; Konigsberg, W.H.; Edelman, G.M. Bidchamister, G. 1171-2181 1970
	DATITIE: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
	A; Reference number: A90564; MUID:71064025; PMID:5530842
	A;Contents: Bu
	A, Accession: A90564
_	A; Molecule type: protein
	A.NOSTBILUGES: 130-1154, Q. 1150-1155, Q. 1150-1156, Q. 11
	R:Ponstincl. H:: Hilschmann, N:
_	Hoppe-Sevler's Z. Physiol. Chem. 357, 1571-1604, 1976
_	A, Title: Die Primaerstruktur eines monoklonalen 19G1-Immunglobulins (Myelomprotein Ni

```
Gypecies: Homo sapiens (man)
Cypecies: Force: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
Cypecies: Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
RyHuck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
AyTitle: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene
AyReference number: A23511; MUID:86148507; PMID:3081877
AyResidues: 1-377 cHUC>
AyResidues: 1-377 cHUC>
AyResidues: 1-377 cHUC>
AyCoss-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
AyGene: GDB:IGHG3
AyCross-references: GB:X119339; OMIM:147120
AyMap position: 14932.33-14932.33
AyIntrons: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
CySuperfamily: immunoglobulin C region; immunoglobulin homology
CyReywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
C;Kesidues: 1-377 < HUCS-
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.8%; Score 1626.5; DB 3 Best Local Similarity 81.7%; Pred. No. 2.4e-86; Matches 308; Conservative 10; Mismatches 12
                                                                   gamma-3 chain C region (allotype G3m(b)) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA--
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ALHNRFTQKSLSLSPGK 377
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A/H1/2 224/1
C/Gomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfied bonds. In some cases, such as IgA and IgM, the subunits associate into la C/Superfamily: immunoglobulin Cregion; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology < IM2>
F/20-65/Domain: immunoglobulin homology < IM2>
F/20-67/Domain: immunoglobulin homology < IM2>
F/20-70/Logo = 208/Disulfide bonds: #status experimental
F/103/Disulfide bonds: interchain (to heavy chain) #status experimental
F/109/III/Disulfide bonds: interchain (to heavy chain)
F/108/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Molecule this sequence has the Glm(3) and Glm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
B; Gordenistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammad-immunoglobulin. X. Intrachain disulfid A; Title: The covalent structure of a human gammad-immunoglobulin. X. Intrachain disulfid A; Title: The covalent structure of a human gammad-immunoglobulin. X. Intrachain disulfide bonds
A; Title: An Contents: Aschwarz, J; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob enbromide cleavage products, and the disulfide bridges.
A; Gontents: annotation; disulfide bonds
A; Gontents: annotation; disulfide bonds
                                                                                                                      A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-34, '0', 36-96, 'K', 98-115, '0', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Note: this sequence has the G1m(17) and G1m(1) markers
A; Note: this sequence has the G1m(17) and G1m(1) markers
A; Schmidt, W.B.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, '713-747, 1963
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A; Reference number: A91723; MUID: 83289131; PMID: 6884994
A; Contents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
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                    A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.7
Matches 329, Conservative
Primaerstruktur
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ઠે 임 ò 요 ò 셤 ò g ò 셤 ò

Sun Apr

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Algeference number: A34591

Blochem: G.; Frangione, B.

Blochem: J. 121, 217-225, 1971

Alfilatein, C.; Frangione, B.

Blochem: J. 121, 217-225, 1971

Alfilatein, C.; Frangione, B.

Algeference number: A30253, 1971

Algerence number: A30253, 1971

Algerence number: A30253, 1971

Algerence number: A30357; MUID: 69064124; PMID: 5782707

Algerence number: A33157; MUID: 69064124; PMID: 5782707

Algerence number: An immunoglobulin heterotetramer: immunoglobulin heterotetramer: immunoglobulin heterotetramer: immunoglobulin homology < IMI>
Fluatorel number: An immunoglobulin homology < IMI>
Fluatorel number: immunoglobulin homology < IMI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 PSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEDYN
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6.8e-85;
thes 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.8%; Score 1600; DB
90.9%; Pred. No. 6.8e-8
ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            447 QOGNVFSCSVMHEALHNHYTQKSLSLSPGK
A,Molecule type: protein
A,Residues: 238-275 <406F-
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 90.9%
Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
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A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q'
A;Note: this sequence has since been revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The amino acid sequences of the three heavy chain constant region domains A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
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                                                                                                                                                                                                                                                                  61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 GFYPSDIAVEWESNGQPENNYKITPPVLDSDGSFFLYSKLIVDKSRWQQGNVFSCSVMHE 459
                                                                               Gaps
                                                                                                                                                              121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT
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                                                                                                                                                                                                                                                                                                                                              ------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
                                                                            47;
                         Length 377;
                                                                         12; Indels
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A; Residues: 1-19, Q',21-57, Z',59,'A',61-193,'D',195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
                                                                                                                                                                                                                                  207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA------
                            DB 2;
                      Score 1624.5; DB 3; Pred. No. 3.2e-86; 10; Mismatches 12,
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Mol. Immunol. 16, 923-925, 1979
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                                                                      Matches 308; Conservative
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                                             Similarity
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                         Query Match
                                                   Local
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RiSymons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 481-889, 1989
A.Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and A.Reference number: S06610; MUID:90097986; PMID:2513487
A.Recession: S06610; MUID:90097986; PMID:2513487
A.Rocession: S06610
A.Molecule type: DNA
A.Residues: 142-470 <SYM>
A.Residues: 142-470 <SYM>
A.Rocessa-references: EMBI:X16701
C.Genetics: the sequence was determined from the germline gene
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S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
R;Patri, S.; Nau, F.
R;Patri, S.; Nau, F.
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Cession: S31459
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
C;Text. (Annother Company Annother C;Text. (Annother C)
                                                                                                                                                                                                                                                                                                                                                                                              A.Gene: Ig CH gamma-1
A.Johntrons: 98/1; 111/1; 221/1
A.Introns: 98/1; 111/1; 221/1
C.Superfamily: immunoglobulin C region; immunoglobulin, membrane protein
C.Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology < IMM:
F;18/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LFSVVGMVYNNWF-DVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOP--E 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNPLWTLLFVLSAPIGVLSQVQLRESGPSLVKPSQTLSLTCTVSGPSLS-SYALTWVRQA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 1567; DB 2; Length 4 63.7%; Pred. No. 8.1e-83; ive 56; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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F;277-346/Domain: immunoglobulin homology <IMM>
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Matches 305, Conservative
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A, Molecule type: protein
A, Residues: 1.30,81-326 cPIN>
C, Genetics:
A, Ge
A;Accession: A90933
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Roldues: 1-327 <ELL>
A;Note: the sequence was determined from the germline gene
B;Note: the sequence was determined from the germline gene
B;Note: the sequence was determined from the germline gene
B;Note: the sequence Patrial amino acid sequence of the constant
A;Title: Human immunoglobulin sublclasses: Partial amino acid sequence of the constant
A;Reference number: A90249; MUID:70207560; PMID:4192699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVFLFPPKFPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
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N.Alternate names: Ig gamma-1 chain C region (clone 8.10)
(Species: Bos primisgenius taurus (cattle)
C.Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Ju
C.Accession: $22080; $06610; Ā31303
R.Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A.Reference number: $22080
A.Accession: $22080
A.Actus: pr&liminary
A.Rocicule type: mRNA
A.Residues: 1-470 <SAN>
A.Residues: 1-470 <SAN>
A.Cross-references: EMBL:X&2916; NID:g439; PIDN:CAA44699.1; PID:g440
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90.6%; Pred. No. 4.1e-84;
:ive 12; Mismatches 16; Indels
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299

306

204 366 264 426

246 144

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Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin homology <IMM> F;276-345/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LKWIGWIYPASGNTKYNENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCAR----A 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIISKAKGQPREPQVYTLPPSKDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 422
                 127 MVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 186
                                                                                                                                                                                                                                                                                                                                                                265 KAKGOPREPQVYILPPSREEMIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 LEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.0%; Score 1426.5; DB 2; Length 469; 57.2%; Pred. No. 9.3e-75; ive 71; Mismatches 121; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 WFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKG 64
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                                                                                                                                                                              247 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                   145 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                 205 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                           367 KAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 WIFLFLLSGTAGVHCQ1QLQQSGPELVKPGASVKISCKASGYTFT-DYYINWVKQKPGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 VGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 LTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 EPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
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                                                                                                187 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP
                                                                                                                                                                                                                                                                                                                                                                                                                      LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                         325 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
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563339
Ig heavy chain V region precursor - human
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: 569339; S7566
R; Khamlichi, A. A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: 569339; MUID:95262687; PMID:7744049
A; Residues: 1-374 «KHA»
A; Residues: BMBL:X81695
B; Khamlichi, A. A.
Submitted to the EMBL Data Library, September 1994
A; Residues: S72664
A; Accession: S72664
A; Accession: S72664
A; Residues: 1-140, C', 142-374 «KH2»
A; Cross-references: EMBL:X81695
C; Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                        64 GLEWIGSFYSSGNTY----YNPSLKSOVTISTDTSKNOFSLKLNSMTAADTAVYYCVR 118
                                                                                                                                                                                                 114
                                                                                                                                                                                                                                        119 DRLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 178
                                                                                                                                                                                                                                                                               173
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                                                                                                Gaps
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                                                                         4 LWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGK
                                                                                                                                                                                61 ALEWIG-----GSGYDEDIDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCAR
                                                                                                                                                                                                                                                         179 FPEPVIVSWNSGALISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNVNHKPSNT
                                                                                                                                                                                                                                                                                                                                           174 MPEPVTVTWNSGALTSGVHTFPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASST
                                                                                                                                                                                                                                                                                                                                                                                                                             DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 DPEVQFSWFVDNVEVRTARTKPREEQFNSTPRVVSALPIQHQDWTGGKEFKCKVHNEALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--
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                                      16;
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               Pred. No. 1e-81;
3; Mismatches 104; Indels
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61.9%; Pic.
                                      Conservative
    Best Local Similarity
Matches 297; Conser
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Ug gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: 501321
R;de Waele, P:; Feys, V; van de Voorde, A.; Molemans, F.; Fiers, W.
Bur. U. Blochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directerance number: 501320; MUID:88329081; PMID:3138116
                                                                                                                                                                                                           Projects: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: Pc4436
E;Accession: Pc4436
E;Accession: Pc4436
E;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp A;Reference number: JCS810; WUID:98063277; PMID:9398605
A;Accession: Pc446
A;Accession: Pc446
A;Accession: Pc446
A;Accession: Pc446
A;Accession: Pc446
A;Accession: Capity (mulb) Pa063277; PMID:9398605
A;Accession: Capity (mulb) Pa063277; PMID:9398605
A;Accession: Capity (mulb) Packetin (capity) (mulb) (
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A,Residues: 1-475 < ABL).
A,Cross-references: BMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A,Note: this sequence was determined from the differentiated gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-2a chain (mAb735) - mouse (5/Species: Mus musculus (house mouse) (5/Species: Mus musculus (house mouse) (5/Species: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999 (5/Accession: 840295 R/Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi A; Reference number: S40295 R/Reference number: S40295 R/Accession: S40295 R/ACCESS R/ACCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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A Map position: 12
Cysterics:
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356 RTISKPKGSVRAPQVYVLPPPBEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 YNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWFDVWGPG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 YNEKFKGKATLIYDISSSTAYMQLSSLISEDSAVYFCARGGKFAM-----DYWGOG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP-- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317
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Fil8-46/Domain: Cregion <CR1>
Fil8-214/Domain: Cregion <CR1>
Fil3-31-340/Domain: Cregion <CR1>
Fil3-340/Domain: Cregion <CR3>
Fil3-340/Domain: Cregion <CR3>
Fil3-446/Domain: Cregion <CR3>
Fil3-446/Domain: Cregion <CR3>
Fil4-446/Domain: Cregion <CR3>
Fil4-446/Domain: Cregion <CR3>
Fil4-446/Domain: Cregion <CR3>
Fil4-446/Domain: immunoglobulin homology <IMM>
Fil4-446/Domain: immunoglobulin homology <IMM>
Fil4-199, 261-321, 367-425/Disulfide bonds: #status predicted
Fil2-96, 144-199, 261-321, 367-425/Disulfide bonds: interchain (to light chain) #status predicted
Fil2-1, 227, 229/Disulfide bonds: interchain #status predicted
Fil2-1, 277, 259/Disulfide bonds: interchain (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.6%; Score 1392; DB 2; Length 446;
57.6%; Pred. No. 8.4e-73;
ive 68; Mismatches 112; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 PAVLQSD-LYTLSSSVIVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 YVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 VLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                              TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                            KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 264; Conservative
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R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from :
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Species: 31-Mar-1980 Hasquence revision 01-Dec-2000 #text change 01-Dec-2000
C;Accession: S25057; A02157; A26232; A26233; A35598
C;Accession: S25057; A02157; A26232; A26233; A35598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TWV) inactivating neotop specific
                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                   61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                                                                                                                                              120 ---QVGLLP---FGYWGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                               1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKKAEPKSCDKT-HTCPP----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                               15;
                                                                                                                                    DB 2; Length 475;
                                                                                                                                 53.7%; Score 1369.5; DB 2; Length ilarity 54.5%; Pred. No. 1.8e-71; Conservative 77; Mismatches 128; Indels
Superfamil : immunoglobulin C region; immunoglobulin homology
                         C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 138-161, 'L', 163-189, 'FP', 193-474 < YAM>
A; Cross-references: GB:JO0461
A; Note: the sequence was determined from the germline gene
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lg gamma-2b chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA; Residues: 1-474 <FIS>
                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A02157
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PGK 475
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                                                                                                                                                                        Matches 263;
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Science 206, 1299-1303, 1979

A; Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he A; Reference number: A26235; MUID:80081501; PMID:117548

A; Rodecusion: A26235; MUID:80081501; PMID:117548

A; Rodecusion: A26235

A; Molecule type: mRNA

A; Residues: 138-172, P, 174-189, FP, 193-376, T', 378-474 <TUI>
A; Tucker, P. W.; Marcu, K. B.; Newell, N.; Richards, J; Blattner, F.R.

A; Tucker, P. W.; Marcu, R. B.; Newell, N.; Richards, J; Blattner, F.R.

A; Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl A; Reference number: A26232; MUID:80081502; PMID:117549

A; Accession: A26232

A; Accession: A26232

A; Rougeon, F.

R; Ollo, R.; Rougeon, F.

R; Ollo, R.; Rougeon, F.

R; Ollo, R.; Rougeon, F.

A; Residues: 138-172, P; 174-189, FP', 193-376, T', 378-474 <TU2>

A; Residues: DAA

A; Reference number: A26233; MUID:82173203; PMID:6803173

A; Contents: b allele

A; Rocession: A26233

A; Molecule type: DNA

A; Residues: 138-161, L', 163-189, FP', 193-300, R', 302-331, A', 333-437, DI', 440-474 <OLL

A; Cross-references: GB:000461

R; Kim, H.; Yamaguchi, Y.; Mascuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takaha:
J; Biol. Chem. 269; 12345-12350, 1994

A; Rittle: O-glycosylation in hinge region of mouse immunoglobulin G2b.

A; Reference number: A55598; MUID:94216359; PMID:7512967
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submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene produc A;Reference number: S31866
A;Reference number: S31866
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A;Residues: 1-255 <FIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 TKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 297
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C,Keywords: immungalobulin
F:1-22/Region: Bscherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region
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49.3%; Score 1256; DB 4; Length 255;
Best Local Similarity 97.1%; Pred. No. 2.8e-65;
Matches 232; Conservative 0; Mismatches 7; Indels
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Job time : 22.3633 secs
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C.Species: Sus selections and the sequence revision. --
C.Date: 21-Feb-1997 #sequence revision. --
C.Date: 21-Feb-1997 #sequence revision. --
C.Date: 21-Feb-1997 #sequence revision. 14715
R.Kacession: 14715
B. Tamunol. 153, 3565-3573, 1994
A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A.Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a S.A. Reference number: 147158; MUD:95015845; PMID:7930579
A.Residues: 1-328 «KAC»
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8,Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
R;Filpula, D.
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Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
411 NGHTEENYKDTAPVLDSDGSYFIXSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISR 470
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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

March 29, 2003, 09:06:23 ; Search time 11.3492 Seconds (without alignments) 1739.566 Million cell updates/sec Run on:

US-09-758-173-12 2549 1 MKHLWFFLLLVAAPRWVLSQ.......MHEALHNHYTQKSLSLSPGK 476 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Maxdal M.J., Belaman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
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MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
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                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=770070269; PubMed=826475;
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MEDINE=71064025; PubMed=5530842;
Rulishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
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Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-1 chain C region.
                                                        330 AA.
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MEDLINE-82274218; PubMed-6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human imm
Nucleic Acids Res. 10:4071-4079(1982).
                                                    PRT;
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PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDBEVKFNMYVDGVEVHNAKTKPREEGYN 326
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.2%; Score 1763; DB 1; 1
Best Local Similarity 99.7%; Pred. No. 1.8e-113;
Matches 329; Conservative 0; Mismatches 1;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
1g gamma-2 chain C region.
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330 AA;
            GC2_HUMAN
P01859;
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                                                                                                                                                                                                  Delsenhofer J.;

Delsenhofer J.;

Delsenhofer J.;

Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus across and 2.9- and 2.8-A resolution.";

Biochemistry 20:2361-2370(1981).

I MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 210-L, KOL & EU SEQUENCES HAVE THE GIM(3) MARKERS THE GIM (NON-1) MARKERS.

I MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,199,269 & 272.

I MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 199, 269, AND 272 AND IN THE ORDER OF RESIDUES
                                                                      Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal
ligdl immunoglobulin (myeloma protein Nie). I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
[0ppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                            -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
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InterPro; IPR003597; Ig cl.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig 3.
SMART; SM00410; IG like; 1.
SMART; SM00407; IGcl; 2.
PR0SITE; PS00290; IGG MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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REMOVED POST-TRANSLATIONALLY.

K -> R (IN GIM(3) MARKER).

/FTIGAVAR 003886.

D -> E (IN GIM(NON-1) MARKER).

FTIGAVAR 003887.

L -> M (IN GIM(NON-1) MARKER).

/FTIGAVAR_003888.
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INTERCHAIN (WITH HEAVY CHAIN)
INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE-81208100; PubMed=7236608;
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HINGE.
CH2.
CH3.
                                                        MEDLINE=77070267; PubMed=1002129;
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Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1FC1; 15-JUL-92.
PDB; 1FC2; 15-JUL-92.
Genew; HGNC:5525; 1GHG1.
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                                          DISULFIDE BONDS
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EMBL; J00230; AAB59393.1; -. PIR; A02148; G2HU.
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Genew, HGNC:5526; IGHG2.
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                                                                                                                                                                                                                          TISSUE=Fetal liver;
MEDLINE=8423992; PubMed=6129676;
MEDLINE=8423992; PubMed=6129676;
Krawinkel U., Rabbitte T.H.,
"Comparison of the hinge-coding segments in human immunoglobulin gamma "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=80001357; PubMed=113060;
Connell G.E., Parr D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human 1962 myeloma protein.";
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"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
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                                              Ellison J.W., Hood L.E.; "Lingon J.W. Hood L.E.; "Linkage and sequence honology of two human immunoglobulin gamma heavy chain constant region genes."; Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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SEQUENCE OF 238-275 (ZIE)
MEDLINE=801419; PubMed=118920;
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human immunoglobulinis gamma chains.";
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[7]
[7]
REVISIONS TO 25; 59, 60 AND 264-268 (ZIE).
Submitted (MAR-1980) to the PIR data bank.
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Wang A.-C., Tung B., Fudenberg H.H.;
"The primary structure of a human 1gG2 heavy chain: genetic, evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
                                                                                                                                                                                                                                                                                                                                                                                                      [5]
SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=69064124; PubMed=5782707; Frangione B., Miletein C., Pink J.R.L.; "Structural studies of immunoglobulin G."; Nature 221:145-148(1969).
                                                                                                                                                                                                                SEQUENCE OF 99-177 AND 310-326 FROM N.A
                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [8] SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A.,
"Characterization of the two unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995)
                       SEQUENCE OF 2-326 FROM N.A. MEDLINE=82197621; PubMed=6804948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=72033500; PubMed=4940472;
                                                                                                               SEQUENCE OF 88-115 FROM N.A.
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NCBI_TaXID=9606
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326 REMOVED POST-TRANSLATIONALLY (PROBABLE)
60 S -> A (IN MYELOWA PROTEINS TIL & ZIE)
/ FTIGA-VAR 003889.
109 C -> S (IN REF. 3).
35884 MW; 8310878C6878CF9C CRC64;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_C1.
InterPro; IPR003500; Ig_like.
PROMO47; ig; 3.
SWART; SM00410; IG_like; 1.
SWART; SM00407; IGC1; 2.
PR051TE; PS00290; IG MHC; 2.
PR051TE; PS01290; IG MHC; 2.
NON_TERF 1.
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   178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                                     SEQUENCE OF 88-266 FROM N.A.
MEDLINE=83299917; PubMed=6193512;
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                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=70110015; PubMed=5461106;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 76910n.
                                                                                                                                                                                                                     323 AA
                                                                                                    447 QOGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                      298 QEGNVFSCSVMHEALHNHYTQKSLSLSK 327
                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
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InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                     STANDARD;
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HSSP: P01857: 1FC1
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P01870;
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                                                                                                                                                                                                                                SEQUENCE OF 1-30 AND 81-326.
MEDLINE=70207560; PubMed=4192699;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=83157104; PubMed=6299662;
BIIson J.W., Buxbaum J.N., Hood L.E.;
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DNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.2%; Score 1586.5; DB 1; Length 327; Best Local Similarity 90.6%; Pred. No. 2e-101; Matches 299; Conservative 12; Mismatches 16; Indels 3;
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INTERCHAIN (WITH A LIGHT CHAIN).
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HINGE.
CH2.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00400; IG_like; 1.
       g gamma-4 chain C region.
GHG4.
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HSSP, P01842, 7FAB.
Genew, HGNC:5528, IGHG4.
                                                Homo sapiens (Human)
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327 AA;
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Gavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                     T -> M (IN D11 MARKER).
N -> A (IN B15 MARKER).
N -> E (IN REF 2).
Q -> E (IN REF 2).
Q -> E (IN REF 3 AND 4).
Q -> E (IN REF 3 AND 5).
Q -> E (IN REF 3 AND 5).
Q -> E (IN REF 3 AND 5).
N -> D (IN REF 5).
N -> D (IN REF 5).
E -> Q (IN REF 5).
N -> D (IN REF 5).
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                  Query Match
48.1%; Score 1226.5; DB
Best Local Similarity 69.7%; Pred. No. 7.6e-77
Watches 228; Conservative 34; Mismatches 5:
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Submitted (APR-1975) to the PIR data bank
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MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
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  IPR003597; 19_cl.
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DISULPIDE BONDS.

MEDLIRE=11058474; PubMed=4922544;
Oliveira B., Lamm M.E.;
Uliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Biochemistry 10:26-31(1971).
Biochemistry 10:26-31(1971).
II. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
13 INBRED GUINEA PIGS.
                                                                                                                                            SEQUENCE OF 69-133 AND 312-329.
MEDIATE=705846; PubMed=5538616;
Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
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"Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE=7503672; Pubmed=4429665;
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"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=75036073; PubMed=4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1212.5; DB 1; Length 329;
; Pred. No. 7.1e-76;
28; Mismatches 63; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 13:4796-4803(1974).
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InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003600; Ig_like.

Pfam; PF00047; ig; 2.

SM0481; SM00410; Ig_like; 1.

SMART; SM00407; IG_like; 1.

PROSITE; PS00290; IG_MHC; 1.
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79
105
107
110
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178
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-I- MISCELLANBOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL GARMA-3 HEAVY CHAINS.
-I- GARMA-3 HEAVY CHAINS.
-I- MISCELLANBOUS: DISEASE PROTEIN OWN MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.
-I- MISCELLANBOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS IS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
                                      384 RDELTKNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLDSDGSFFLYSKLTV 441
                                                            176 QYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPS 235
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-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAYY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE=81021548; PubMed=6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
"Primary structure of human gamma 3 immunoglobulin deletion mutant:
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-82247835, PubMed-6808505,
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=77118561; Pubmed=402063;
Michaelsen T.E., Frangione B., Franklin E.C.;
Primary structure of the 'hinge' region of human 1gG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=77021516; PubMed=823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin B.C.; The amino acid sequence of 'heavy chain disease' protein SUC. Structure of the Fc fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC)
                                                                                                                       DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
                                                                                                                                           296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene deletion model.
                                                                                                                                                                                                                                                                   GC3 HUMAN
P01860;
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QV -> EB (IN ZUC).
YFT1G=VAR 003890.
P -> L (IN OMM).
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F -> Y (IN OMM).
/FIId=VAR 003896.
E69CBC95705B2F46 CRC64;
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INTERCHAIN (WITH HEAVY
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T -> A (\overline{IN} OMM).

/FTIG=VAR 003893.

S -> N (\overline{IN} OMM).
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Y (IN OMM).
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20; Mismatches
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MISSING (I
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/FTId=VAR
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CH2.
CH3.
                                                                              EMBL, J00231; AAAS2805.1; ALT_SEQ.
PIR, A02149; G3HUWI.
                                                                                                                                        MIM, 147120;
InterPro; IPR003006; Ig MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_like.
Pfam; PP00047; ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IgC1; 1.
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Genew; HGNC:5527; IGHG3.
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| Brueggemann M.; | Brolution of the rat immunoglobulin gamma heavy-chain gene family."; | Bruegemann M.; | Broluti, | Brootof, | Bran. | Brothat; | Prop. | Brootof, | Ig_cl. | Bran. | Brothat; | Brootof, | Ig_cl. | Bran. | Brothat; | Brootof, | Ig_cl. | Immunoglobulin domain; | Immunoglobulin domain; | Immunoglobulin domain; | Immunoglobulin | Immuno
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371 OFREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 430
                          18S QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSD 244
                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-1 chain C region.
Rattus norvegicus (Ratl).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 383
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013BAB45EF49B9DA CRC64;
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                                                                                                                                       24S GSFFLYSKLTVDKSRWQQGNIFSCSVWHEALHNRFTQKSLSLSPGK 290
                                                                                                       431 GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=89232738; PubMed=3149946;
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                                                                                                                                                                                                                                                                                              STANDARD;
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326 AA;
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P20759;
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family."; gene 74:473-482(1988).
PIR; PS0018; PS0018.
HSSP; P01842, 7PRB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003500; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 GPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKS-----CDKTHTCPPCPA 260
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                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.8%; Score 1142.5; DB 1; Length 333; ilarity 63.7%; Pred. No. 4.3e-71; Conservative 44; Mismatches 69; Indels 9;
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SMART; SM00410; IG 1ke; 1.

SMART; SM00400; IG-1; 2.

PROSITE; PS00290; IG-MC; 1.

Immunoglobulin domain; Immunoglobulin C region.

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IS INTERCHAIN (WITH A
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-28 chain C region.
Rattus norvegicus (Rat)
             444 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                              PRT;
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                                                                                              STANDARD;
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214; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE=80012837, PubMed=113776;
RSGGETS J., Clarke P., Salesr W.;
"Sequence, analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDLINE-8020559; PubMed=6765952;
Obbata M., Yamawaki-Kataoka Y., Tskahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
                                                                                                          19 gamma-1 chain C region.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evolution of immunoglobulin subclasses. Primary structure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=73008889; PubMed=5073237;
SvaetL J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 6:3305-3321(1979).
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MEDLINE=78242288; PubMed=98524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine myeloma gammaī chain.";
J. Biol. Chem. 253:6068-6075(1978).
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00793; CAA24176.1; --
EMBL; V00795; CAA24176.1; --
EMBL; A02159; GAA2
HSSP; P01842; 7FAB.
GlycoSuiteDB; P01868; --
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_Cl.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGcl; 2.
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                                          STANDARD;
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                                                                                                                                                                                                                                                                                gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                          NCBI_TaxID=10090;
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                                       GC1 MOUSE
P01868;
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           RESULT 9
GC1 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL 264
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                                                                                                                                                                                                                                                                                                                                                                          44.6%; Score 1138; DB 1; Length 324;
62.0%; Pred. No. 8.5e-71;
ive 55; Mismatches 61; Indels 10; Gaps
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MEDLINE=85027161; PubMed=6092053;

Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

Tucker P.W., Blattner F.R.;

"Structural analysis of the murine IgG3 constant region gene.";

EMBO J. 3:2041-2046(1984).
                                                                                                                                 INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                  REMOVED POST-TRANSLATIONALLY.
                                                                                                                                                                                                                                                                                  324 324 REMOVED POST-TRANSLATIONAN
276 276 N -> D (IN REF. 3).
278 278 N -> D (IN REF. 3).
324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mus musculus (Mouse).
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276
Alternative splicing.
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P22436;
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=8222190; PubMed=6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Naka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Indels 10; Gaps
SEQUENCE OF 323-393 FROM N.A. MEDILINE=82197626; PubMed=6804950; Tyler B.W., Cowmann A.F., Gerondadis S.D., Adams J.M., Bernard O. "MRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
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                                                                                                                                                                                                                                                     Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl Eisenberg D., Wall R.; Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; Cell 26:19-27(1981).
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4CC88343B7A1CE27 CRC64;
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HINGE.
CH2.
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EMBL; V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
PIR, B02159; GINSM.
HSSP; P01842; 7FAB.
MGD; MGI:96446; IGh-4.
InterPro; IPR003006; IG_MHC.
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393 AA;
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Best Local Similarity
Matches 205; Conserv
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     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568 (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 FYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-IPKPSTPPGSSCPPGNILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCP--PCPAPELLG
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NON_TER 1 1 7 CH1.

DOMAIN 98 113 HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1137; DB 1; Length 329;
Pred. No. 1e-70;
46; Mismatches 69; Indels
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
1g gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse)
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                                                                                                  EMBL; J00451; -; NOT_ANNOTATED_CDS.
PIR; B02156; G3MSC.
HSSP; P01857; IFC1.
INTERPRO; IPR003006; Ig_AHC.
INTERPRO; IPR003609; Ig_11ke.
INTERPRO; IPR003609; Ig_11ke.
SMART; SM00417; Igc1.
SMART; SM00410; IGC1, 2.
PROSITE; PS00290; IG_MHC; 1.
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HINGE.
CH2.
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P01869;
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GCIM MOUSE
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GCAA MOUSE
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1 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD
                                                             GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMART; SM00410; IG_like; 1.
SWART; SM00407; IG_l; 2.
SPROETE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
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15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-3 chain C region, membrane-bound form.
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Nucleic Acids Res. 11:6775-6785(1983).
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EMBL; V01526; CAA24767.1; ALT_SEQ
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HSSP; P01857; 1FC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003600; Ig_like.
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P03987;
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Yamawaki-Kataoka Y., Miyata T., Honjo T.;
'Yencomplete nuclectide sequence of mouse immunoglobin gamma 2a gene
and evolution of heavy chain genes: further evidence for intervening
sequence-mediated domain transfer.";
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MEDLINE=81223894; PubMed=6787604;
MEDLINE=81223894; PubMed=6787604;
%Con R., Auffray C., Morchamps C., Rougeon F.;
%Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain gen suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                          60 FYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-IPKPSTPPGSSCPPGNILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 NSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 OMSKKKVSLTCLVTNFFSEAISVEWERNGELEODYKYTPPILDSDGTYFLYSKLTVDTDS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                          69; Indels
                                                                                                                                                                                                                                                                            Length
                                                                                                                                                  E -> G (IN REF. 2).
E -> Q (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
CH1.
HINGE.
CH2.
CH3.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                         Query Match 44.2%; Score 1126; DB 1;
Best Local Similarity 63.8%; Pred. No. 7.2e-70;
Matches 210; Conservative 46; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 03, Last annotation update)
1g gamma-2A chain C region, A allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 WQQGNVFSCSVMHEALHNHYTQKSLSLSP 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 9:1365-1381(1981)
                                                                                                                                                                                                                           43929 MW;
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97
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     SEQUENCE FROM N.A.
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                                                                                                                                                         Bourgois A., Fougereau M., Rocca-Serra J.; "Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function."; Eur. J. Biochem. 43:423-435(1974).
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                              Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
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                                                                                        MYELOWA PROTEIN MOPC 173.
MEDLINE=74175517; PubMed=4831970;
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DISULFIDE BONDS.
MEDLINE-73056887; PubMed=4565406;
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InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003600; Ig_like.
Pfam; PF00047; ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_1; 2.
PROSITE; PS00290; IG_MHC; 1.
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112
144
250
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330 AA;
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DISULFID 27
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"Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Igla and Iglb allotypic forms.";

Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

-1- MISCELIANEGUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK-----SCDKTHTCPPCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6;
MEDLINE=82037861; PubMed=6170065;
Schreder P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D "Multiple differences between the nucleic acid sequences of 19G2aa and 19G2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.9%; Score 1119.5; DB 61.3%; Pred. No. 1.6e-69; ive 52; Mismatches 71
                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g gamma-2A chain C region, B allele.
                                                                                                                                                                                              $
299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00479; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=8203777; PubMed=6794027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_C1.
Interpro; IPR003500; Ig_like.
Pfam; PF00047; Ig; 3.
SWART; SM00410; IG_like; 1.
PR08RT; SM00407; IGC1; 2.
PR0SITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 61.3*
Matches 206; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A02153; G2MSAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01842;
                                                                                                                                                                                       GCAB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 HREDYNSTLRVVSALPIQHQDWASGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239
                                                                         PPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLT 440
                                                                                                     Eukaryotang (Modes).
Eukaryotan Metezoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN).
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01.-NUG-19901 (Rel. 19, Last sequence update)
15.-UU.-1999 (Rel. 38, Last annotation update)
19 gamma-2A chain C region, membrane-bound form.
                                                                                                                                                                                                 300 VQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK 335
                                                                                                                                                                       VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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INTERCHAIN
INTERCHAIN
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PIR; A02154; G2MSAM..
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MGD; MGI:9644; Igh-1.

InterPro: IPR00306; Ig MHC.

InterPro: IPR003597; Ig-cl.

InterPro: IPR003597; Ig-like.

Pfam; PF00047; ig; 2.

SMART; SM00410; IG_like; 1.

SMART; SM00407; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                              STANDARD;
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1112
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1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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01-AUG-1991
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                                                                                                                                                                                                                                                                        61 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118
                                                                                                                                                                                                                                                                                                                                       265 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 324
                                                                                                                                                                                                                                                                                                                                                                  325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKABPKSCDKTHTCPP--CPAPELL
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                                          43.8%; Score 1117; DB 1; Length 399; 63.4%; Pred. No. 3e-69; ive 43; Mismatches 74; Indels
399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;
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Job time : 13.3492 secs
                                                               Best Local Similarity 63.49
Matches 210; Conservative
  SEQUENCE
                                               Query Match
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(without alignments)
2271.829 Million cell updates/sec
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2549
1 MKHLWFFLLLVAAPRWVLSQ........MHEALHNHYTQKSLSLSPGK 476
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: sparchas:\*
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7: sp\_namman:\*
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10: sp\_vertebree:\*
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13: sp\_vertebree:\*
14: sp\_unclassified:\*
15: sp\_archas:\*
17: sp\_archas:\*

SPTREMBL 21:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q8tc77 homo sapien	Q8tc63 homo sapien	Q991c4 mus musculu	Q9d814 mus musculu	Q8r3v9 mus musculu	Q9rla4 mus musculu	Q99131 mus musculu	Q99125 mus musculu	Q8r3h6 mus musculu	Q91z05 mus musculu	Q96pq8 homo sapien	Q95m34 equus cabal	Q96ey0 homo sapien	Q9bul0 homo sapien	Q9bqb8 homo sapien	homo
SUMMARIES		ID	Q8TC77	QBTC63	Q99LC4	Q9D8L4	Q8R3V9	Q9R1A4	Q99L31	099125	Q8R3H6	091205	Q96PQ8	Q95M34	O96EY0	Q9BU10	09BQB8	Q8WUX4
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	* Query	Match	82.5	81.4	57.8	56.4	56.3	56.1	55.6	54.7	53.6	53.6	49.7	49.5	38.2	37.2	37.1	36.8
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096AA6 096EB9 096EB9 099EB9 099M22 099M24 091X92 096A68 091WP5 091WP1 099WA4 091WT1 099WA4 091WT1 099WA4 091WT1 099WA4 099WP6 099WP6 099WP6 099WP6 099WP6 099WP6	PRT; Created) Last sed Last ann Creatian; Crania Catarr SABBL/Gen SABBL/Gen	SCORE 210 PICAL NO. 16; Mismat. GPGLVKPSETL GGGLVKPGSL OVTISTDTSKN OVTISTDTSKN SASTKGPSVPP
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Mus musculus (Mouse)
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                                                                                                                                                                                                                Q99LC4
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                                                                                                                                       RESULT 3
Q99LC4
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TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK 238
                                                                 244 AEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 303
                                                                                                            239 VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 298
                                                                                                                                                                                                            FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 363
                                                                                                                                                                                                                                                           FINNYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 358
                                                                                                                                                                                                                                                                                                                                                        TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 423
                                                                                                                                                                                                                                                                                                                                                                                                  68 PPGKGLEWIGTI-NFSGNMYYSPSLRSRVTWSADMSENSFYLKLDSVTAADTAVYYCAAG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 HL--VMGFGAH-----WGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 PEPVIVSWNSGALISGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNIK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 PPGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 RLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 VDKRVESK---YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVVSOED 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSI-SGGYGWGWIRQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 MKHLWFFLLLLVAAPRWVLSRLQLQESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
Hypothetical 52.0 kDa protein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC025983, AAH25985.1;
Hypothetical protein.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
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TISSUE=KIDNEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 YYSY-----DLFAYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
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56.3%; Pred. No. 1.9e-109;
ive 84; Mismatches 108; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKHLWFFLLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
R HSSP; PO1042; 7FAB.
R HSSP; PO1042; 7FAB.
R InterPro; PR003599; 1g-1.
R InterPro; PR003599; 1g-1.
R InterPro; PR003599; 1g-1.
R InterPro; PR003506; 1g-MHC.
R InterPro; PR003506; 1g-MHC.
R InterPro; PR003506; 1g-MHC.
R SMART; SM00409; 1G-1.
R SMART; SM00409; 1G-1.
R SMART; SM00406; 1G-1.
R SMART; SM00410; 1G-1.
R S
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UNN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                               463 AA
                                                                                                                                                                                                                                                                                                                                         PRT;
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Matches 269; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                    475 GK 476
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MEDLINE-SIOBSE60; Pubbed=11217851;

Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Asiawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Puruno M., Anno H., Baldarelli R., Barsh G.,

Brownstein M.J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Austani Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-P.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashi, Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
                                                                                                         Created)
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003600; Ig.like.
InterPro; IPR003000; Ig.like.
InterPro; IPR003596; Ig.like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
                                                                                                   01-JUN-2001 (TrEMBLrel. 17,
01-DUN-2001 (TrEMBLrel. 19,
18100600991k procedu.
IGH-1 OR 18100600991K.
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Matches 269; Conservative
                                                    PRELIMINARY;
                                                                                                                                                                                                                                          Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                               Q9D8L4;
                                                    Q9D8L4
RESULT 4
Q9D8L4
                                                                                                         DDA BERNARD BRANK 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
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241 DKKAEPK-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 294
                                                                                                                                295 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 354
                                                                                                                                                                      415 QPENNYKTĮPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 474
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                  232 DKKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVD
                                                                                                                                                                                                                                                                                                                  352 RALPSPIEKTISKPRGPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNG
                                                                                                                                                                                                                                                                         355 KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC024405.1; -. Hypothetical protein. SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical 52.0 kDa protein. Mus musculus (Mouse).
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
               410 AENYKNIQPIMDIDGSYFVYSKINVQKSNWEAGNIFICSVLHECLHNHITEKSLSHSPGK 469
417 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 NPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWFDVWGPGV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 PAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 TVPEV---SSVFIFPPKPKDVLTITLTPRVTCVVVDISKDDFEVQFSWFVDDVEVHTAQT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
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                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.1%; Score 1430.5; DB 11; Length 437; 58.3%; Pred. No. 4.9e-106; Live 72; Mismatches 96; Indels 23;
                                                                                                                                                                                                                                                                                            Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF12372; AAD40243.1; -...
HSSP, P01842; 7FAB.
MGD; MGI:9646; Igh-4.
InterPro; IPR003506; Ig_MRC.
InterPro; IPR003596; Ig_V.
EMART; SM0047; ig; 4.
SMART; SM00410; IG_like; 2.
SWART; SW00410; IG_like; 2.
SWART; SW00410; IG_like; 2.
SWART; SW00410; IG_like; 2.
SWART; SW00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                     PRELIMINARY;
                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                              NCBI_TaxID=10090;
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NON TER
SEQUENCE
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61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 -----LLYGGYYDYWGQCTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EPVTVSWNSGALTSGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKKARPKSCDKTHTCPP -- CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 NYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 468
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.6%; Score 1416; DB 11; Length 468; 56.7%; Pred. No. 7.7e-105; ive 68; Mismatches 127; Indels 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Letron (FEB-2001) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. R HSSP; P01842; 7FAB.

R HSSP; P01842; 7FAB.

R InterPro; IPR003599; Ig.

R InterPro; IPR003500; Ig_like.

R InterPro; IPR003506; Ig_MHC.

R InterPro; IPR003566; Ig_V.

R SMART; SM00409; Ig.; 2.

R SMART; SM00409; IG.; 2.

R SMART; SM00409; IG.; 2.

R SMART; SM00409; IG.; 1.

R SMART; SM00410; IG.; 1.

R SMART; SM00410; IG.; 1.

R PROSITE; PS00290; IG. MHC; UNKNOWN 1.
                                                                                                                                                                                       099L31;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
millar to RIKEN CDNA 1810060009 gene.
400 LNVQKSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 271; Conservative
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                              RESULT 7
Q99L31
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RESULT 8

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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 -----GSIYYGYGLYYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LFSVVGMVYNN----WFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 NTKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.7%; Score 1394.5; DB 11; Length 473; 55.8%; Pred. No. 4.1e-103; Live 71; Mismatches 127; Indels 15;
                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ffam; PF00047; ig; 3. SMART; SM00409; IG; 2. SMART; SM00409; IG; 2. SMART; SM00406; IG; 13. SWART; SM00410; IG like; 1. SWART; SM00410; IG like; 1. PROSITE; PS00290; IG MHC; UNKNOWN 1. SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                   Last sequence update)
Last annotation update)
                    473 AA
           099L25
099L25
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequent of June 2002 (TrEMBLrel. 21, Last annote Similar to RIKEN CDNA 1810060009 gene.

Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; PO1842; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig. cl.
InterPro; IPR003600; Ig. Mic.
InterPro; IPR003596; Ig. Mic.
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                              SO DE REPRESENTATION OF THE PROPERTY OF THE PR
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RESULT 9 Q8R3H6

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180 NSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 SCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 IGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LFLLSVTEGVHSQVQLLQSGPELVKPGASVKISCRASGYAFSKSW-MNWVKRRPGKGLEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 KDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                               53.6%; Score 1367; DB 11; Length 474; 54.8%; Pred. No. 6.5e-101; tive 75; Mismatches 124; Indels 16.
                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; ECO26447; ARH25447.1; -. Hypothetical protein. BRS EQUENCE 474 AA; S1748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC010327; AAH10327.1; -.
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 AA
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Mus musculus (Mouse)
                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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18; Gaps

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MEDLINE=99383416; PubMed=9717671;
MEDLINE=99383416; PubMed=9717671;
MEDLINE=99383416; PubMed=9717671;
Magner B., Oversech G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant region genes. II. Aligament of c-mu, c-gamma, c-epsilon and c-alpha genes.";
Immunobiology 199:105-119(1998).
EMBL, AJ30675; CAC44624.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
RNGSITE; PS00290; IG_MC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS---NTKVD 241
                                                                                                                                                                                                                                                                                                                                                                                                            422 VSWGQGCATVG-----HFGVY-----TRVSQYIEWLQKLMRSEPRPGVLLRAPFP 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 701
                                                                                                                                                                                                                                                                                                       49.7%; Score 1268; DB 4; Length 701; 82.7%; Pred. No. 9.1e-93; tive 4; Mismatches 29; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magner D.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                    77826 MW; 94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region
                                                                    SMART; SMOOIG1; EGF; 2.

PROSITE; PSOOIG1; EGF; 2.

PROSITE; PSOOIG1; ASX HYDROXXL; UNKNOWN 1.

PROSITE; PSOIG22; EGF-1; UNKNOWN 1.

PROSITE; PSOIG167; EGF-2; UNKNOWN 1.

PROSITE; PSOOIG1; GLU CARBOXYLATION; UNKNOWN 1.

PROSITE; PSOO290; IG WHC; UNKNOWN 1.

PROSITE; PSOO134; TRYPSIN DOM; 1.

PROSITE; PSOO134; TRYPSIN DOM; 1.

PROSITE; PSOO135; TRYPSIN HIS; UNKNOWN 1.

HYDROSITE; PSOO135; TRYPSIN SER; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 337 AA
Pfam; PF00008; BGF; 2.
Pfam; PF00594; gla; 1.
Pfam; PF00047; ig; 2.
Pfam; PF00089; trypain; 1.
SWART; SM00181; EGF; 2.
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 82.7
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment).
                                                                                                                                                                                                                                                                                                         Query Match
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"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunorherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).
EMBL, AF272774; AAK56866.1; -..
EMBL, AF272774; AAK5686.1; -..
InterPro; IPR000152; Asx. hydroxyl.
InterPro; IPR000152; BGF 2.
InterPro; IPR001081; BGF-1.ke.
InterPro; IPR001081; BGF-Ca.
InterPro; IPR001254; SGF Ca.
InterPro; IPR001254; SGF Drotease_Try.
InterPro; IPR001254; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                       67 WIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVG 126
                                                                                                                                                                                                                                                                                                                            127 MVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 186
                                                                                                                                                                                                                                                                                                                                                                                             WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 KSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHED 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIEKTISKAKGOPREPQVYTLPPSRDELTXNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEEN 416
                                                                                                                                                           Similarity 55.6%; Score 1365.5; DB 11; Length 473; Similarity 55.6%; Pred. No. 8.5e-101; 55. Conservative 70; Mismatches 123; Indels 19; Gaps
                                                                                                                                                                                                                                                       7 FILLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 YKTTPPVLDSDGSFFLXSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 MGD; MGI:2144967; AU044919.
InterPro; IPR0010345; CytC heme_bind.
InterPro; IPR001006; Ig_MFC.
Pfam; PF00047; ig; 3.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096P08,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Factor VII active site mutant immunoconjugate.
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MEDLINE=21477448; Pubmed=11593034;
                                                                                                                                                                                Best Local Similarity 55.6%
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                             Query Match
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352 MCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH 409
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                                                     318 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKÇKVSNKALPAPIEKTISKAKGQP-REPQ 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                   179 FPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNH 233
                                                                                                                                                                                                                          232 PNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREG 291
                                                                                                                                                                                                                                                                                                                                                                    292 KQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137.2%; Score 948.5; DB 4; Length 597;
llarity 37.5%; Pred. No. 2.4e-67;
Conservative 76; Mammerches 176; Indels 113; Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
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                                                                                                                                                         234 KPSN-----TKVDKKAEPKS-----CDKTHTCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.

I Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.

R HSSP, P01825; 7AAH02963.1; -..

R InterPro; IPR001359; Ig.
R InterPro; IPR001359; Ig.
R InterPro; IPR0013560; Ig_MHC.
R InterPro; IPR0013060; Ig_MHC.
R InterPro; IPR001306; Ig_WHC.
R SWART; SM00440; IG; 2.
SWART; SM00440; IG; 2.
SWART; SM00440; IG; 1.

R SWART; SM00410; IG 11ke; 1.

R SWART; SM00410; IG 11ke; 1.

R PROSITE; PS00290; IG MHC; UNKNOWN_3.
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SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         530 RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                               257 -----PCPAPELLGGPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical 65.3 kDa protein. Homo sapiens (Human).
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                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AGKGLEWIGRIY-TSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCASQP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 WELPTVGLFY-----WGQGTLVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDF 172
                                                                                                                                                                                                                                                                                                                                                                    207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEP-----KSCDKTHTCPPCPA 260
                                                                                                                                                                                                                                                                                                                                                                                                          61 GFYSLSSWYTVPASTWTSETYICNVVHAASNFKVDKRIEPIPDNHQKVCDMS-KCPKCPA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
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                                                                                                                                                                                                                      147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.2%; Score 973; DB 4; Length 613;
llarity 38.5%; Pred. No. 2.8e-69;
Conservative 75; Mismatches 163; Indels 120; Gaps
                                                                                                                                                                                                                                                                    1 ASTTAPKVFALAPGCGTTSDSTVALGCLVSGYFPEPVKVSWNSGSLTSGVHTFPSVLQSS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKHLWFFLLLLVAAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSIS-SYYWSWIRQP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                     6
                                                                                    DB 6; Length 337;
                                                                            Query Match
49.5%; Score 1262.5; DB 6; Length
Best Local Similarity 69.2%; Pred. No. 9e-93;
Matches 234; Conservative 42; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO11857; AAH11857.1;
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam: PF00047; Ig; 5.
SWART; SM00408; IGc2; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin domain.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
               337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 LSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSKNPGK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown (protein for MGC:20337)
Homo sapiens (Human).
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SEQUENCE
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Q96EY0
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358 CVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRONGEAVKTHT 415
121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYF 179
                                        238 NGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGK 297
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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InterPro; IPR003599; Ig.
InterPro; IPR003500; Ig_like.
InterPro; IPR003600; Ig_like.
InterPro; IPR003506; Ig_v.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
InterPro; IPR0047; ig; 5.
SMART; SM00407; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00410; IG; 1.
SMART; SM00410; IG_like; 1.
SMART; PS00290; IG_MHC; UNKNOWN 3.
SPQUENCE :597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; AAH06180.1; -.
EMBL; BC001872; AAH01872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown (protein for MGC:1905) (protein for MGC:1228).
Homo sapiens (Human).
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TISSUE=MUSCLE;
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37.1%; Score 944.5; DB 4; Length 597;

Query Match

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17;
Best Local Similarity 37.5%; Pred. No. S.1e-67;
Matches 219; Conservative 75; Mismatches 177; Indels 113; Gaps
                                                                                                                                                          61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                    60 PGKGLEWIGEL-NHSGITNYNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVI 118
                                                                                                                                                                                                                                                 121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                           180 PEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHK 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 NGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGK 297
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                                                                                              1 MKHLWFFLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFS-GYYWSWIRQP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 CVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHT
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Job time : 45.1716 secs
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Sequence 12, Application US/10124905

Patent No. US20020166136A1

GENERAL INFORMATION:
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Abexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22114

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: TEEKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-836-2021
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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USA
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Sequence 250, App
Sequence 43, Appl
Sequence 25, Appl
Sequence 68, Appl
Sequence 216, Appl
Sequence 216, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Appl
Sequence 12, Appl
Sequence 4, Appli
Sequence 6, Appl
Sequence 66, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 14, Appl
                                                                                                                                       March 29, 2003, 09:14:52; Search time 18.2478 Seconds (without alignments) 1531.829 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 222,
Sequence 224,
Sequence 39,
                                                                                                                                                                                                                                                US-09-758-173-12
2549
1 MKHLWFFLLLVAAPRWVLSQ........MHEALHNHYTQKSLSLSPGK 476
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-948-429B-12
US-09-948-429B-4
US-09-925-179-66
US-09-925-179-66
US-09-920-171-14
US-09-920-171-14
US-09-96-28B-25
US-09-96-28B-25
US-09-96-28B-25
US-09-96-28B-25
US-09-96-28B-25
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US-09-96-28B-21
US-09-96-28B-21
US-09-96-28B-21
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US-09-96-28B-22
US-09-96-28B-22
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Maximum Match 100%
Listing first 45 summaries
                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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APP 1

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Sequence 244,
Sequence 216,
Sequence 240,
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Sequence 248,
10 US-09-796-848A-41

0 US-09-996-288-220

10 US-09-996-288-226

9 US-09-996-288-255

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10 US-09-996-288-234

9 US-09-996-288-234

10 US-09-996-288-234

10 US-09-996-288-212

10 US-09-996-288-214

10 US-09-996-288-24

10 US-09-996-288-24
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## ALIGNMENTS

012712-131

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Gaps

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Sequence 4, Application US/10124905

Patent No. US20020166136A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "HARNACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS ITLE OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
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                                                                                                                                                                                                                                                                                                                   Length 476;
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100.0%; Pred. No. 2.6e-129;
ive 0; Mismatches 0;
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699 Prince Street
                                                                                   012712-131
                                                                           REFERENCE/DOCKET NUMBER: 0127
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
                                                               35,030
     FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                            Matches 476; Conservative
                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                              Similarity
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Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PMARWACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANS, SWECKER & MATHIS
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                                                                                                                                                                                                                                                                                                                   LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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                                                                                           100.0%; Score 2549; DB 9;
100.0%; Pred. No. 2.6e-129;
ive 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
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APPLICATION NUMBER: 09/383,916
                                                                                       Query Match
Best Local Similarity 100.
Matches 476; Conservative
                               // MOLECULE TYPE: protein
US-10-124-905-12
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                 linear
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CLASSIFICATION:
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                 TOPOLOGY:
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TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDP 300
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90.6%; Score 2309; DB 9; Length 47
Best Local Similarity 91.2%; Pred. No. 1.7e-116;
Matches 434; Conservative 9; Mismatches 33; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                 APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY, AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
FREFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
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                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-10-124-905-4
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                       FILING DATE:
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US-09-948-429B-4
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181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
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                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBERS OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-09-948-429B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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80 YNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNW-FDVWGP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 QVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTY 79
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                                                             APPLICANT: Lownsan, Henry B.
APPLICANT: Presets, Leonard G.
APPLICANT: Davids Deals M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FITE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REPRENCE: P11.2G2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT APPLICATION NUMBER: US 08/887,352
PRIOR RILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 451;
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7. OTHER INFORMATION: Heavy chain sequence derived from MAE11
18-09-920-171-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

83.4%; Score 2126; DB 10; Length
Best Local Similarity 87.6%; Pred. No. 9.6e-107;
Matches 401; Conservative 17; Mismatches 32; Indels
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
FILE REFERENCE: P0718P2CIDICIUS
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
FRIOR APPLICATION NUMBER: US 08/466,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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Sequence 18, Application US/09920171
Patent No. US20020054878A1
GENERAL INFORMATION:
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Sequence 65, Application US/09925179
Publication No. US20030044858A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 18
LENGTH: 451
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US-09-925-179-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 FPAVLQSSGLYSLYSTSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
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83.4%; Score 2127; DB 9; Length 451;
Best Local Similarity 87.6%; Pred. No. 8.5e-107;
Matches 401; Conservative 18; Mismatches 31; Indels
                                                                               Sequence 66, Application US/09925179
Publication No. US20030044858A1
GENERAL INFORMATION:
APPLICANT: Jaddau, Paula M.
APPLICANT: Preser, Leconard G.
TITLE OF INFORMATION: Anti-1gE Antibodies (as amended)
FILE REFERENCE: P0718P2CIDICIUS
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/85,899
PRIOR PILING DATE: 1995-03-15
PRIOR PELING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
LENGTH: 451
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                                      RESULT 5
US-09-925-179-66
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US-09-920-171-18
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APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardiau, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 1997-07-02
PRIOR FILING SATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                      Length 451;
                                                                                                                                                                                                                                                                                                                  Query Match
Bost Local Similarity 87.3%; Score 2124; DB 10; Length 4
Bost Local Similarity 87.3%; Pred. No. 1.2e-106;
Matches 400; Conservative 19; Mismatches 31; Indels
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                                                                                                                                                                                                    CTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-920-171-14
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                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                  PRIOR FILING DATE: 1999-04-21
                                                        NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
LENGTH: 451
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Best Local Similarity
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LENGTH: 451
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APPLICANT: Lownan, Henry B.
APPLICANT: Lownand G.
APPLICANT: Lownand G.
APPLICANT: Lownand G.
APPLICANT: Lown, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REPERSENCE: P1123C108
FILE REPERSENCE: P1123C208
FILE REPERSENCE: P1123C208
FILE REPERSENCE: P1121CAN NUMBER: US 09/920,171
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR APPLICATION NUMBER: US 09/296,005
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83.3%; Score 2124; DB 9; Length 45
Best Local Similarity 87.3%; Pred. No. 1.2e-106;
Matches 400; Conservative 19; Mismatches 31; Indels
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PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR FILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR APPLICATION NUMBER: PCT/US92/06860

PRIOR FILING DATE: 1992-08-14

PRIOR FILING DATE: 1992-06-07

PRIOR FILING DATE: 1992-06-07

PRIOR PLING DATE: 1992-06-07

PRIOR PRILING DATE: 1991-08-14

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 68
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Patent No. US20020054878A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophyl
TITLE OF INVENTION: and Treatment
FILE REPERBNCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILIAG DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 250
                                                 173 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC 232
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                                                                                                                                                                                                                                                                                                                                                                                                 413 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450
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CORGANISM: Homo sapiens
US-09-996-288-250
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Patent No. US20020177126A1

GREEAL INFORMATION:

GREEAL INFORMATION:

APPLICANT: Young, James

APPLICANT: Scott, Koenig

APPLICANT: Goott, Koenig

APPLICANT: Lealie, Johnson

TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi

TITLE OF INVENTION: and Treatment

TITLE OF INVENTION: and Treatment

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 259

SOFTWARE: Patentin Version 3.1

SEQ ID NO 218
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                                                                                                                                                                                                    PPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
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83.3%; Score 2122.5; DB 9; Length 450;
Best Local Similarity 87.3%; Pred. No. 1.5e-106;
Matches 400; Conservative 18; Mismatches 31; Indels 9;
Query Match 83.3%; Score 2124; DB 10; Length 451; Best Local Similarity 87.3%; Pred. No. 1.2e-106; Matches 400; Conservative 19; Mismatches 31; Indels 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 LIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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LENGTH: 475
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-925-179-68
      US-09-740-002-25
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Matches
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                                                                                                                                                                                  Sequence 43. Application US/09796848A
Patent No. US2002008189A1
GENERAL INFORMATION
APPLICANT: Young, James F.
APPLICANT: Johnson, Leelie S.
APPLICANT: Wu, Herren
APPLICANT: Wu, Herren
APPLICANT: Wat Hersen
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: High Potency
TITLE OF INVENTION: WAT HERSEN BEASON-256
CURRENT APPLICATION NUMBER: US. 60/186,252
PRIOR APPLICATION NUMBER: US. 60/186,252
PRIOR APPLICATION NUMBER: US. 60/186,252
RUMBER OF SEQ ID NOS: 59
SSOTUM RE: Patentin Ver. 2.1
SSOTUM O 43
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 YYNPSLKSQVTISTDTSKNOFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWFDVWGP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 GVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Heavy chain of OTHER INFORMATION: high potency antibody.
US-09-796-848A-43
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83.3%; Score 2122.5; DB 10; Lengt
Best Local Similarity 87.3%; Pred. No. 1.5e-106;
Matches 400; Conservative 18; Mismatches 31; Indels
                                                                 413 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450
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ORGANISM: Artificial Sequence
                                                                                                                                              RESULT 12
US-09-796-848A-43
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RESULT 13

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Sequence 25, Application US/09740002;
Fatent No. US20020001798A1
GENERAL INFORMATION:
TOUR THE NORTON: PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
THE REFERENCE 1091-00-12-20
TRICK APPLICATION NUMBER: 09/335,697
PRIOR FILLING DATE: 1999-06-18
PRIOR FILLING DATE: 1999-06-07
SOFTWARE PARENT ON NUMBER: 09/488,376
PRIOR FILLING DATE: 1995-06-07
SOFTWARE PARENT ON NUMBER: 09/488,376
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NOS: 27
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246 KSCDKTHICPPCPAPELLGGBSVFLFPPKPKDTLMISRIPEVTCVVDVSHEDPEVKFNM 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LFLVAVATRVLSQVQLQESGPVVVKPTETLTLTCTVSGFSLSNPRMGVTWIRQPPGKALE 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Indels
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
FILE REPERBNCE: P0718P2C1DICIUS
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/466,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%; Score 2122.5; DB 10
ilarity 86.4%; Pred. No. 1.5e-106;
Conservative 20; Mismatches 41;
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Gaps

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112 198 172 258 232 292

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79 YYNPSLKSQVTISTDTSKNOFSLKLNSMTAADTAVYYCVRDRLFSVVGMVYNNWFDVWGP 138
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                                                                                                           Query Match 83.2%; Score 2120.5; DB 9; Length 450; Best Local Similarity 87.3%; Pred. No. 1.9e-106; Matches 400; Conservative 18; Mismatches 31; Indels 9;
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                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-216
          LENGTH: 450
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Patent No. US20020177126A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Young, James

APPLICANT: Lealie, Johnson

TITLE OF INVENTION: Mchods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi

TITLE OF INVENTION: and Treatment

FILE REFERENCE: 10271-047-999

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 259

SOFTWARE: Patentin version 3.1

SEQ ID NO 216
                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table US-09-925-179-68
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PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-07
PRIOR PLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
LENGTH: 451
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial sequence
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Perfect score:
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linear

DNA

ALIGNMENTS

Sequence 11 from patent US 6113898.

RESULT 1
AR108867
LOCUS
DEFINITION
ACCESSION

AR108867.1 GI:12825143

Unknown. Unknown

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

Unclassified.

1 (bases 1 to 1431)

Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C. Human B7.1-specific primatized antibodies and transfectomas expressing said antibodies
Patent: US 6113898-A 11 05-SEP-2000;

A07562 DNA sequenc BC026038 Homo sapi I26929 Sequence 3

Homo sapi

A29585 HSIGGIKH MACIGHVCDR AK097010

1359

1624

1121.2 1121.2 1116.2 1115.6

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1112 1108.2 1107.6 1106.2 1103.8

AR108865

AR135377 Sequence
AR135376 Sequence
BC024289 Homo sapi
AR042589 Sequence
AR042589 Sequence
AR419496 Sequence
AX419496 Sequence
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AX419737 Homo sapien
BD000501 Process E
BC018747 Homo sapien
AR07859 Homo sapien
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BC01904 Homo sapien
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AK05816 Homo sapi
AK057775 Homo sapi
AK03189 Sequence
AK097365 Homo sapi
AR135375 Sequence
AR135377 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES AR076262 AX330501 AX333307 AX334122 HUMIGHEPAH BC019046 AK098817 AR135376 BC024289 AR031184 AR042589 AR076260 AX419496 HSIGG1LH BD000501 AR059284 AR135377 В 112999 112999 112999 112999 112999 112999 1430 1673 1507 Length 1633 % Query Match I 1181 1177.8 1176.2 1134.8 1134 1134 1133.8 1131.8 1130.6 1125.2 1125.2 1125.2 1125.2 1122.8 1122.8 1122.8 1213.6 1182.8 1142.6 1134.8 1134.8 8

FEATURE BO BASE CO ORIGIN	RES Location/Qualifiers source 1. 1431 COUNT 319 a 462 c 385 g 265 t	Qy 961 CGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCACCGTCCTCACCGTCTGCACCAG 1020
Quer Best Mato	<pre>Juery Match 100.0%; Score 1431; DB 6; Length 1431; Sest Local Similarity 100.0%; Pred. No. 4.5e-279; Atches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	1021 GACTGGCTGAATGCCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC
දු දු	1 ATGAAACACCTGTGGTTCTTCCTCCTCGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60	OY 1081 ATCGAGAAAACCATCTCCAAAGGCCAGCGGCGGCGGGAACCACACGTGTACACCCTG 1140
රු සි	61 GTGCAGCTGCAGGACTCGGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120	Qy 1141 CCCCCATCCCGGGATGACCTGACCAGAACCAGGTCAGCCTGACCTGGTCAAAGGC 1200
<i>상</i>		OY 1201 TTCTATCCCAGCGACATCGCCGTGGAGAGCAGCCAGCCGGAGAACAACTAC 1260
රු පු	181 CCAGGGAAGGGCTGGAGTTGGGAGTTTCTATAGTAGTAGTAGGAACACCTACTAC 240 	Oy 1261 AAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTTCCTCTACAGCAAGCTCCC 1320
දු පු	241 AACCCCTCCCTCAAGAGTCAAGATCACATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300 241 AACCCTCCCTCAAGAGTCAAGATCACCATTTCAACAAGACACGTCCAAGAACCAGTTCTCC 300	Qy 1321 GTGGACAAGAGCAGCAGCAGCAGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
දු පු	ო ო	QY 1381 CTGCACAACCACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
Эр	361 CTITITICAGITGTIGGAAIGGITIACAACAACIGGITCGAIGICIGGGGCCCGGGAGIC 420 	AR108863
÷ 6	421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTTTCCCCCTGGCACCCTCC 480	TION Sequence 3 from patent US ION AR108863 GI:12825139 N AR108863.1 GI:12825139 DS
ò q	481 TCCAAGAGCACCTCTGGGGGCACAGGGGCCCTGGGTGAGGACTACTTCCCC 540 	
<b>상</b> 임	541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCG 600	AUTHORS Anderson, D.R., Brams, P., Hanna, N., Sheetowsky, W.S. and Heard, C.  TITLE Human B7.1-specific primatized antibodies and transfectomas expressing said antibodies  JOURNAL Patent: US 6113898-A 3 05-SEP-2000;
<u>ن</u> و	601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660	FEATURES Location/Qualifiers  Source 11431  Acranism="unknown"  BASE COUNT 322 a 469 c 380 g 260 t
දු පු	661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720 	/ Match 91.9%; Score 1315.8; DB 6; Length 1431; Local Similarity 95.0%; Pred. No. 8.5e-256;
% q	721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACATGCCCACGTGCCCAGCA 780 	Matches 1359; Conservative 0; Mismatches 72; Indels 0; Ga 1 AIGAAACACCIGIGGITCIICCICCICGIGGCAGCICCCAGAIGGGICCIGICCAG
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è 8	901 GAGGTCAAGTTCAACTGGTACGTGGACGGGGGGGGGGGCGAAATGCCAAGACAAAGCCG 960 	Db 121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTGGACCTGGATCCGCCAGACC 180 Qy 181 CCAGGGAAGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTGGGAACACCTACTAC 240

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              CTGAAGCTGAACTCTATGACCGCGCGCACACGGCCGTGTATTACTGTGTGAGAGATCGT
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1 (bases 1 to 1567)

Hillman,J.L., Lal.P., Tang,Y.Tom., Yue,H.,
Corley,N.C., Guegler,K.J. and Baughn,M.R.
Human immune system associated molecules
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/product='heavy chain of human monoclonal FT
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JP 1996038178-A ZO 13-FEB-1996;

MATIBODY AND PRODUCTION THEREOF, AND

JP 1996038178-A ZO 13-FEB-1996;

OS Homo aspiens (human)

PN JP 1996038178-A/ZO

PD 11-FEB-1996

PR 19-FEB-1995 JP 1995030742

PR 20-FEB-1995 JP 1995030742

PR 19-FEB-1995 JP 199503074

PR 19-FEB-1995 JP 199503074

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/cell_type='B cell'
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/product='signal peptide of heavy chain of human monoclonal antibody against human cytomegalovirus 65kD
                                                                                                                                      HUMAN MONOCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR CLONTING OF GENE THEREOF
PACENT: JP 1996038178-A 20 13-FEB-1996;
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/product='heavy chain of human monoclonal
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Best Local Similarity 93.9%; Pred. No. 9.2e-245;
Matches 1347; Conservative 0; Mismatches 78; Indels 9;
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1 (bases 1 to 1431)
Tanaka,S., Niwa,H. and Tanaka,H.
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RESULT

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                                                 mRNA linear PRI 27-MAR-2002 clone CBL01928, highly similar to
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Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL01928
Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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87.8%; Score 1256.8; DB 9; Length 1594;
Best Local Similarity 93.8%; Pred. No. 7.1e-244;
Matches 1345; Conservative 0; Mismatches 77; Indels 12;
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NEDO human cDNA sequencing project
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CGGGA 417  CGGGA 446  CGGGA 446  CACCC 477  CACCC 506  CACTC 537  CACTC 537	CCTTC 597 (CCTTC 626 CCTTC 657 (CTCC 657 CCTCC 686	CCAAG 717       . CCAAG 746 CGCCA 777 	(CAGCC 1077 	ACACC 1137               ACACC 1166   CAAA 1197   CAAA 1226   CAAA 1226   CAAAA 1257
358 CGTCTTTTTCAGTTGGAATGGTTTACAACTGGTTCGATGTCTGGGGCCCGGGA  193 TGGTTCCTGGGGTTCTGGAGTGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGA  184 TGTGTTCTTTCCTCTGGGGTTGCTGTTGTTGTTCTCCCTGGGCCCGGGG  185 TGGGTTCCTGGTTCCTCTGGGTAGCTAGGCCCTTGGTTTTCCCCTGGGCCCGGGG  186 TCTCTGGTCCTGGCGCCCTCTCGCGCCCTGGGCCTTTTCCCCCTGGGCCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCTGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGCCTGCCTGGCCTGGCCTGGCCTGGCTGCT			B CCTGAGGTCAAGTTCAACTGGTACGTGGGGGGGGGGGGG	CCCATGGAGAAACCATCTCCAAAGCCAAAGGCAGCCCGAGAACCAGGTGTACACC
Oy     358       Db     393       Oy     418       Db     447       Oy     478       Db     507	Oy 538 Db 567 Oy 598 Db 627		Oy 898 Db 927 Oy 958 Db 987 Oy 1018 Db 1047	0y 1078 Db 1107 Oy 1138 Db 1167 Oy 1198

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1596 bp mRNA linear PRI 15-JUL-2002 Homo sapiens CDNA FLJ25650 fis, clone SYN01104, highly similar to AK098516
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Ono,Y., Horuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S.,
Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
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Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (108-JUL-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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Oligo capping; fis (full insert sequence).
Oligo capping; fis (full insert sequence).
Homo sapiens synovial membrane (knee) cDNA to mRNA, clone_lib:SYN
clone:SYN01104.
HOMO sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                          1347 ACCGTGGACAGAGCAGGTGGCAGGGAACGTCTTCTCATGCTCGTGATGCATGAG 1406
1227 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC 1286
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                                                                                         1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCTC
                                                                                                                                                                                                                                                                           1318 ACCGTGGACAAGAGCAGGTGGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
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/clone_Tib="synovial membrane (knee)"
/clone_Tib="synovial membrane (knee)"
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NEDO human cDNA sequencing project
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GGAC	ACCAC	ATTGC 	STCAC	) 	STTT   ATACC	AGCAC 	ACAGO	VACTO	YICTA TICTA	VICTO      VICTO		CAGT	DE LE	TGGA 	CGTA       CGTA	ACAA	CCAA	CCAA
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for Location/Qualifiers
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Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL03624.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugano, S. and Suzuki, Y.
Sugano, S. and Suzuki, Y.
Direct Submission

Submitted (24-0CT-2001) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                 1290 TACAAGACCACGCCTCCCGTGCTGGACTCCTCCTTCTTCTTCTACAAGCACCACGCTCCTACAGCAAGCTC 1349
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                                       1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC 1317
86.4%; Score 1236.8; DB 9; Length 1589;
93.0%; Pred. No. 7.8e-240;
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Pred. No. 2.1e-237;
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Edelman,L., Margaritte,C., Kaczorek,M. and Chaabihi,H.
Bodolman,L., Margaritte,C., Kaczorek,M. and Chaabihi,H.
Bodolool, Natur RECOMBINANT ANTI-RHESUS D (D7C2) ANTIBODY
Patent: WO 9607740-A 7 14-MAR-1996;
PASTEUR INSTITUT (FR)
Other publication FR 2724182 960308.
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PAT 17-DEC-2001 'n 1261 CCCGTGCTGGACTCCGACGGCTCCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGC 1320 1201 GACATCGCCGTGGAGTGGGAGAGAATGGGCAGCGGGAGAACAACTACAAGACCACGCCT 1260 312 246 73 GAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCT 132 132 192 189 252 306 372 432 420 492 480 493 TCTGGGGGCACAGCGGCCCTGGGCTGCTCAAGGACTACTTCCCCGAACCGGTGACG 552 72 12; Gaps 13 IGGTICTICCTCCTCCTGGTGGCAGCTCCCAGGTCCTGTCCCAGGTGCAGCTGCAG 72 13 TGTATCATCCTCTTCTTGGTAGCACACTACAGGTGTCCACTCCCAGGTCCAACTGGAG 133 GGTGGTCCTTCA---GTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGG 253 AAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAAC 247 AAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAACTGAAC 433 TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 1273 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTACAGCAAGCTCACCGTGGACAAGAGC 73 cadiodedecadedarionidaadecincedadacecenerecereacerearen GGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGG TCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGTCTTTTTTCAGTT 190 cricia de contra de comente - - a arcaractica a conceacida de concerción de contra 373 GTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTCCTGGTCACCGTC 364 ---TGGAAGTATCATGGGGACTGGTTCGACCCCTGGGGCCAAGGTACCACTGTCACCGTC Query Match

84.8%; Score 1213.6; DB 6; Length 1418;
Best Local Similarity 92.5%; Pred. No. 3.8e-235;
Matches 1312; Conservative 0; Mismatches 94; Indels 12; 1 (bases 1 to 1418)
Edelman, L., Margaritte, C., Kaczorek, M. and Chaabihi, H.
Monoclonal recombinant anti-rhesus D (D7C2) antibody
Patent: US 6312690-A 7 06-NOV-2001;
Location/Qualifiers linear DNA AR176296 1418 bp Sequence 7 from patent US 6312690. AR176296.1 GI:17918651 /organism="unknown" 379 g 454 C Unclassified. 332 a Unknown.

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Isogai, T. and Yamanoto, J.

Direct Submission

Direct Submission

Direct Submission

E. Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & J'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HXI and RAB.

RAB; annotation: HXI and RAB.
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GDPLVDSHHYWAWIRQQPGKGLEWIGHINSYAYKRYNGSLESRLSMSMDTSRNQFSLK
MTSVTDVDTAVYFCALFKSTWFDPWGPGTLVIVSSASTKGPSVFPLAPSSKSTSGGTA
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PETCVVVDVBHEDPBVKFRTWYDGVEVNNKATFRREQYNSTRVDYSTRVDYLTVLHGDWL
NGKSYKKKVSNKALDAPIENTITSAKGQPREPOVTLEPSRDELTKWQVSLTCLLWGF
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                                                                                                                               Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamateu, A., Ishii, S.,
Kamamoto, J., Isono, Y., Kawai, Hio, Y., Satto, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
NEDO human cDNA sequencing project
Unpublished
                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="synovial membrane tissue from rheumatioid
arthritis"
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0; Mismatches 97; Indels 33; Gaps
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  CDNA to mRNA, clone_lib:SYNOV2 clone:SYNOV2001300.
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/note="cloning vector: pME18SFL3"
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/protein_id="BAC05021.1"
/db_xref="G1:21757093"
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/db_xref="taxon:9606"
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oligo capping; fis (full insert sequence).
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1 (bases 1 to 1404)
Hanna,N., Newman,R.Anthony. and Reff,M.Elliot.
Recombinant anti-CD4 antibodies for human therapy
Patent: US 6136310-A 7 24-OCT-2000;
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Pred. No. 1.5e-228;
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Sequence 7 from patent US 6136310.
AR135375
AR135375.1 GI:14476047
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FEATURES Location/Qualifiers  source 11404  Ary Caranism="unknown"  BASE COUNT 313 a 447 c 379 g 265 t  ORIGIN	Query Match 82.3%; Score 1177.8; DB 6; Length 1404; Best Local Similarity 90.3%; Pred. No. 6.6e-228; Matches 1292; Conservative 0; Mismatches 112; Indels 27; Gaps	0y 1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60	QY         61 GIGGAGCTGCAGGACTCGGGCCCAGGACTGAGGCCTTCGGAGACCCTGTCCCTCACC 120	9y 121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180	QY         181 CCAGGGAAGGGGCTGGAGTGGATTGGGATTCTATAGTAGTAGGAACACCTACTAC 240           Db         181 CCAGGGAAGGGACTGGATTGGATTCTATGGCAGTGGGGGGGCACCAATTAC 240	Oy 241 AACCCTCCTCAAGAGTCAAGTCACATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300	Oy 301 CTGAAGCTGAAGCTCTATGACGGCGGGACACGGCGTGTATTACTGTGTGAGAGATCGT 360	OY 361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420  Db 359TATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGAGTC 402	Qy         421 CTGGTCACCGTCTCCTCAGGTAGCACCCATCGGTCTTCCCCCTGGCACCCTCC 480	Qy	Qy         541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACTTCCCG         600           bb         523 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCACCTTCCCG         582	Qy 601 GCTGTCCTACAGACTCTACACCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660	0y 661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGACCCAAGAACACCAAGGTG 720 [	Oy 721 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACAGGCCCACCGTGCCCAGCA 780	Db 754 CCTGAGTCGGGGGGACCGTCAGTCTCTCTTCCCCCCAAAACCCAAGGACACCCTC 840	QY         841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTCGAGGCCTC 900           L	Oy 901 GAGGTCAAGTTCAACTGGTACGTGGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960
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              CGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG
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                                                                                                                                                                                                       Unclassified.

1 (bases 1 to 1404)

Hanna,N., Newman,R. Anthony. and Reff,M.Elliot.

Recombinant anti-CD4 antibodies for human therapy

Patent: US 6136310-A 9 24-OCT-2000;

Location/Qualifiers
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Pred. No. 1.4e-227;
0; Mismatches 113; Indels
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ARquence 9 from patent US 6136310.
AR135376.1 GI:14476048
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Best Local Similarity 90.2%;
Matches 1291; Conservative
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Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA, complete cds.
BC024289
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ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Danes Samilus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1630)

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GTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/tissue type="Spleen"
/clone lib="NIH MGC 113"
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/note="Vector: pOTB7"
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MGC.
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VMHEALHNHYTQKSLSLSPGK"
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Pred. No. 8.4e-221;
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Brams, P., Chamat, S.Salim., Pan, L.-Z., Walsh, E.E., Heard, C.Janne. and Newman, R.Anthony.
Neutralizing high affinity human monoclonal antibodies specific to RSV F-protein and methods for their manufacture and therapeutic use thereof
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Db 1271 CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1330
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1334 GGTGGCAGCAGCAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393	1331 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGCTCTGCACACACA
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OY 1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
Db 1391 ACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428

Search completed: April 6, 2003, 01:56:18 Job time : 4493.25 secs

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                                                                     5, 2003, 19:47:34 ; Search time 65.1566 Seconds (without alignments) 6735.375 Million cell updates/sec
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         version 5.1.3
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Listing first 45 summaries
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Sequence 11, Application US/08487550

Sequence 11, Application US/08487550

Patent No. 6113898

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSED: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWAREN PRICATION DATA:
APPLICATION NUMBER: US/08/487,550
FLING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: TEEKTAION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION INFOR
                      PCT - USSSE - 09576 - 3
US - 08 - 157 - 101A - 9
US - 08 - 149 - 0950 - 3
US - 08 - 476 - 275 - 2
US - 08 - 476 - 275 - 2
US - 08 - 475 - 815B - 3
US - 08 - 475 - 815B - 3
US - 09 - 023 - 715 - 2
US - 09 - 023 - 715 - 2
US - 09 - 027 - 449 - 68
US - 09 - 027 - 449 - 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
MOLECULE TYPE: peptide
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Matches 1411, Conservative 100.04, Fred. No. 0, Indels 0, Gaps 0;  Matches 1411, Conservative 100.04, Mismatches 0; Indels 0, Gaps 0;  1 Althachter 1411, Conservative 100.04, Mismatches 0; Indels 0, Gaps 0;  1 Althachter 1411, Conservative 100.04, Mismatches 100.04, Mismatches 1411, Conservative 100.04, Mismatches 1411, Mismatc	Db 1021 GACTGGCTGAATGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCACACCAC	GENERAL INFORMATION: APPLICANT: Anderson, Darrell R. TITLE OF INVENTION: "MONKEY MONOCLO) TITLE OF INVENTION: TO HUMAN B7.1 A TITLE OF INVENTION: IMMUNOSUPRESAN NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSES: ACTATE: WAS CITY: Alexandria STRET: 699 Prince Street CITY: Alexandria STRET: 699 Prince Street CITY: Alexandria STRET: 699 Prince Street CITY: Alexandria STRET: 099 Prince Street COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Patentin Release #1.0, COMPUTER PREDICATION DATA: APPLICATION NUMBER: US/08/487.550 FILING DATE: O1-JUN-1995 ATTOMENY APPLICATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 35,030 REGISTRATION NUMBER: 35,030 TELEPHONE: 703-836-6620 TELEFRAY: A131 BASE PAIRS TYPE: MUCIPIC ACIG STRANDEDNESS: NOT relevant TOPPLOATY: Linear MOLECULE TYPE: peptide FEATURE: NAME/KRY: CDS LOCATION: 1.1431 FEATURE: NAME/KRY: mat_Peptide
	Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps  1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGAGCTCCCAGATGGGTCCTGTCCCAG 60  1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGAGCTCCCAGATGGGTCCTGTCCCAG 60  1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGAGCTCCCAGATGGGTCCTGTCCCAG 60  61 GTGCAGCTGCTGGTGGTCTTCCTCCTCGTGGAGCTCCTGGAGCTCTGTCCCAG 60  61 GTGCAGCTGCTGGTGGCTCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120  121 TGCGTGTCTCTGGTGGCTCATCAGGAGTGGTTATGGCTTCGGAGACCCTGTCCCTCACC 120  122 TGCGCTGTTCTTGGTGGCTCATCAGGAGTGGTTATGGCTGGAGACCCTGTCCCTCACC 120  123 TGCGCTGTTCTTGGTGGCTCATCAGGAGTGGTTATGGTTGGGAACCCTGTCCTACC 120  124 TGCGCTGTTCTTGGTGGTCGCTCATCAGGAGTTCTATAGTAGTGGGAACCCTACTAC 240  185 CCAGGGAAGGGGCTGGAGTGGATTGGAGTTTTCTATAGTAGTGGGAACCCTACTAC 240  186 CCAGGGAAGGGGCTGGAGTGAGTTTCTATAGTAGTAGTAGTGGAACCCTACTAC 240  187 CCAGGGAAGGGGCTGGAGTGAGTTTCTATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	12

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AND/OR B7.2 PRIMATIZED FORMS THEREOF,
COMPOSITIONS CONTAINING, AND USE THEREOF AS
ANTS"
                      CAGCCCCAAAACCACAGGTGTACACCCTG 1140
                                                                     CAGGTCAGCCTGACCTGCTGGTCAAAGGC 1200
                                                                                                                     IGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCAGCCCCC 1080
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NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUICATION INPORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
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                                                                                     1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCACCTCCCAGATGGGTCCTGTCCCAG 60
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                                       DB 3; Length 1431;
                                                              72; Indels
                                    Score 1315.8; DB 3
Pred. No. 4.4e-308;
0; Mismatches 72;
                                      91.9%;
                                                Best Local Similarity 95.0
Matches 1359; Conservative
; LOCATION: 1..1431
US-08-487-550-3
                                      Query Match
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1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAAGCCCTCCCAGCCCCC 1080 1081 ATCGAGAAAACCATCTCCAAAGGCAAAAGGGCAGCCCCGAGAACCACGTGTACACCCTG 1140 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1260 AAGACCACGCCTCCCGTGCTGGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCAC 1320 1321 GrdGACAAGAGCAGGAGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380 961 CGGGAGGAGCAGTACAACAGCACGTACCGTGGTCAGCGTCCTCACCGTCCTGCACCAGC 1081 ATCGAGAAAACCATCTCCAAAGCCAAAGGGAGCCCCGAGAACCACAGGTGTACACCCTG 1140 1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCAGCCCCC 1381 CIGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431 1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431

Sequence 17, Application US/09049672A
Sequence 17, Application US/09049672A
Settle No. 613594
SETTLE COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536 3: Incyte Pharmaceuticals, Inc 3174 Porter Drive

1205 1197

1077

1017

1317 1385 1377

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906 CTCATGATCTCCCGGAACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGGCCACGAAGAC 965
                                                                   966 CCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAG
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                                           898 CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAG
                                                                                                                          958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC
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ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: MACZOREK, MICHEL
APPLICANT: CHAZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS
TITLE OF INVENTION:
NUMBER OF SUGUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
SSOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT PAPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INPORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08793450 Patent No. 6312690 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON
STATE: VA
COUNTRY: USA
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US-08-793-450-7
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                                                                                                                                                                                                                            Query Match

89.2%; Score 1276.4; DB 3; Length 1567;
Best Local Similarity 94.7%; Pred. No. 1.4e-298;
Matches 1358; Conservative 0; Mismatches 61; Indels 15;
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTER.STICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                    TOPOLOGY: linear

HAMBDIATE SOURCE:

LIBRARY: PANCTUT01

CLONE: 1513264

US-09-049-672A-17
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                                                                                           901 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGGAGGAGGAG 960
                                         661 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAAGCA 720
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          CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGA
                                                                        733 GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG
                                                                                                                                       GGGGGACCGTCATCCTTCCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG
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Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Newman, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 699 Prince Street CITY: Alexandria STREET VA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 84.8%; Score 1213.6; DB 4; Length 1418; Best Local Similarity 92.5%; Pred. No. 1.8e-283; Matches 1312; Conservative 0; Mismatches 94; Indels 12;
                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide

LOCATION: 58..1418

OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY

OTHER INFORMATION: CHAIN"

US-08-793-450-7
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-320
TELEFAX: 703-413-320
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid FEATURE:
                                                                                                                                                                                                                                                               NAME/KEY: sig_peptide
LOCATION: 1..57
FEATURE:
                                                                                                                                                                                                                                 LOCATION: 1..1418
FEATURE:
                                                                                                                                                                    linear
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
CHROMOSOME/SEGMENT: 4
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82.5%; Score 1181; DB 3; Length 1404;
Best Local Similarity 90.4%; Pred. No. 1.3e-275;
Matches 1294; Conservative 0; Mismatches 110; Indels 27
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: OG-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESKID, RODIN L.
REGISTRATION NUMBER: 35,030
FEDERARIC TOOKET UNBER: 35,030
FELERARY: 703-836-6620
TELEPHONE: 703-836-6620
FELERARY: 703-836-6620
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Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Therapy NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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                                                                                      TCCAAGAGCACCTCTGGGGGCACAGGGCCCTGGCTGGTCAAGGACTACTTCCCC
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Pred. No. 7.8e-275;
0; Mismatches 112; Indels 27;
                            CUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: O6-SEP 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION OF RED ID NO: 11:
SEQUENCE CHARACTERISTICS:
LEMOTH: 1404 Dase pairs
TYPE: Nucleic acid
STRANDENESS: single
TYPE: Nucleic acid
STRANDENESS: single
TOTAL THE COUNTY INFORMATION:
MATERIAL THOSE
STRANDENESS: single
TOTAL THOSE
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': 699 Prince Street
Alexandria
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Best Local Similarity 90.3%;
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POSITION IN GENOME:
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MOLECULE TYPE: DN
ORIGINAL SOURCE:
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LOCATION:
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LOCATION:
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Sequence 9, Application US/08523894 Patent No. 6136310

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Pred. No. 1.9e-274;
0; Mismatches 113; Indels 27;
               GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Inerapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
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                                                                                                                                                                                                                                                                                                                                                                  COMPUTER KEADABLE FORM:

MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.30
SOGTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-58P-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-2021
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
CHARACTERISTICS:
                                                                                                                                                                                                      ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.2%;
Best Local Similarity 90.2%;
Matches 1291; Conservative (
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1..1404
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
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LOCATION:
FEATURE:
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US-08-523-894-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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430 493 490 553 550 613 610 673

us-09-758-173-11.rni

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CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1330
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                                                     254 AGAGCAGACTCACCACCTCCCAGGACACCTCCAGAAGCCAGGTGGTCCTAAGCTTCACCA
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                                                                                                                  Sequence 17, Application US/08488376

Patent No. 5811524

GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, ROLand Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUWAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
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Pred. No. 1.8e-264;
0; Mismatches 147; Indels 9;
CTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAATGA 1404
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET:
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM
MEDIUM TYPE: FORM
MEDIUM TYPE: FORM
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 89.0
Matches 1262; Conservative
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; LOCATION:
US-08-488-376-17
                                                                                     RESULT 8
US-08-488-376-17
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1151 ATGAGCTGACCAAGAACCAGGTCAGCCTGACTGCCTGCTAAAGGCTTCTATCCCAGCG 1210
  GCTC---CATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGC
                         137 TCTCACTCAGCAACCCTAGAATGGGTGTGACCTGGATCCGTCAGCCCCCCGGGGAAGGCCC
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                                                                                      374 TIGGAAIGGIIIACAACAACIGGIICGAIGICIIGGGGCCCGGGGAGICCTGGICACCGICI
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APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Jahn
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
ANDIES OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
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Pred. No. 1.8e-264;
0; Mismatches 147; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,223
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                    1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMUNICATION INFORMATION:
TELEPAN: (703) 836-6620
TELEPAN: (703) 836-5201
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 14.28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                   ; Sequence 17, Application US/08634223
; Patent No. 5840298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 89.0%;
Matches 1262; Conservative
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; LOCATION:
US-08-634-223-17
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                            17 TCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTCCTGTCCCAGGTGCAGTTGCAGAGT
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ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCGGAGAACAACTACAAGACCACGCCTC
                    ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
                                                                     CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAAGAGCA
                                                                                        CGGGCAGGACGGCTCCTTCTTCCTCTACAGCACACGCGGGACAAGAGCA
                                                                                                                                        GGTGGCAGCGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
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89.0%; Pred. No. 1.8e-264;
.ive 0; Mismatches 147; Indels 9;
                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/08634224

Sequence 17, Application US/08634224

GENERAL INFORMATION:
APPLICANT: GRAMS, Peter
APPLICANT: GRAMST, Soulaima Salim
APPLICANT: WALSH, Bedward Edward Edward Edward APPLICANT: HARSP, Cheryl Janne
APPLICANT: HARSP, Cheryl Janne
APPLICANT: HARSP, Cheryl Janne
APPLICANT: HOWMAN, Roland Anthony
TITLE OF INVENTION: MONOCLOAL ANTIBODIES SPECIFIC TO RSV
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THEE
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #1.30
                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: Z2313-1404
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OCTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELLICATION: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTATION UNDERS: 35,030
REFERENCE/DOCKET WUMBER: 012712-150
REFERENCE/DOCKET WUMBER: 012712-150
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
TELEFAX: (703) 836-2021
TELEFAX: (703) 836-2021
SEQUENCE CHARACTERISTICS:
FENERAL 1428 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 89.0
Matches 1262; Conservative
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; LOCATION:
US-08-634-224-17
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                                                                                          Length 1428;
                                                                                       Score 1134.8; DB 2; Length
Pred. No. 1.8e-264;
0; Mismatches 147; Indels
                                                                                 79.3%;
                                                                                                     Best Local Similarity 89.0 Matches 1262; Conservative
                      CDS
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                   ; NAME/KEY:
; LOCATION:
US-08-634-400-17
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APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: WEMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERRAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                      1333
                                                                                                                                                                                                                                                                                                      1390
                   1091 TCTCCAAAGCCAAAAGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1150
                                                                                     ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG 1210
                                                                                                                                                      CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1330
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1153
                                                                                                                                  ACATCGCCGTGGAGTGGGAAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
                                                                                                                                                                                                                                                                   GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393
                                                                  ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/634,400
                                                                                                                                                                                                                                                                                                                                  ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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P.O. Box 1404
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/488,376
FILING DATE: 07-UTN-1995
ATTORNEY AGENT INFORMATION:
NAME: TESKIN, RODAI L.
REGISTRATION NUMBER: 35,030
FEFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-634-400-17; Sequence 17, Application US/08634400; Patent No. 5939068; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: Virginia
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77 CGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGGTG 136
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                                                                                                                                                                                                                                                  Length 1428;
                                                                                                                                                                                                                                         Query Match 79.3%; Score 1134.8; DB 2; Length Best Local Similarity 89.0%; Pred. No. 1.8e-264; Matches 1262; Conservative 0; Mismatches 147; Indels
           TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                          1..1428
                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-635-878-17
                                                                                                                                                     FEATURE
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APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: WALSH, Edward E.
APPLICANT: WEWANN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STRET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                        974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGGTGAATG 1033
                                                                                        1031 GCAAGGAGTACAAGTGCAAGAACAACAACAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1090
                                                                                                                                        TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACGTGTACACCCTGCCCCCATCCCGGG 1153
                                                                                                                                                                                                           ATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGCG 1213
                                                                                                                                                                                                                                                                                 ACATCGCCGTGGAGGGAGAGGATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
                                                                                                                                                                                                                                                                                                       1211 ACATCGCCGTGGAGTGGGAGGGCATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1270
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                                                                    GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTTCCCAGCCCCCATCGAGAAAACCA
                                                                                                                                                                                                                                                                                                                                                      CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGGAAGCTCACCGTGGACAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1391 ACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAATGA 1428
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREJICATION NUMBER: 08/488,376
PILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08635878; Patent No. 5955364; GENERAL INFORMATION:
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US-08-635-878-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 AGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAACT 313
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              FILING DATE: 07-07195
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE TRARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         1..1428
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US-08-770-057-17
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Patent No. 5958765
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: MEMBAN, Roland Anthony
TITLE OF INVENTION: MONOCLONAL ANTHRODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPBUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1033
                                                                                                                                                                                                        1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAGAAAACCA 1090
                                                                                                                                                                                                                                                                                                                                                                                           1091 TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1150
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                     854 CCCCTGAGGTCACATGCGTGGTGGACGTGAGCCCACGAAGACCCTGAGGTCAAGTTCA
                                                                                        914 ACTGGTACGTGGACGCCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
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                                                                                                                                                                                                                                                                    1034 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
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: United States
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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PRIOR APPLICATION DATA:
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US-08-770-057-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.3%; Score 1134.8; DB 4; Length 1428; Best Local Similarity 89.0%; Pred. No. 1.8e-264; Matches 1262; Conservative 0; Mismatches 147; Indels 9;
        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,697B
FILING DATE: 06-Jul-2000
CLASSIFICATION - Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA: APPLICATION NUMBER: 08/770,057
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELERAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..1428
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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PAN, Li-Zhen
WALSH, Edward E.
HEARD, Cheryl Janne
NEWMAN, Roland Anthony
INVENTION: NBUTRALIZING HIGH AFFINITY HUMAN
MONOCLOVAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
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850
                                                                                                       CCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
                                                                                                                                                                                   911 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGGAGGAGGAGTAATGCCAAGACAAAGCCGCGGGGAGGAGGAGCAGT
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                                                                                  GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCTCATGATCTCCCGGA
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ADDRESSE: Burns, Doane, Swecker & Mathis STRET: P.O. Box 1404
CITY: Alexandria STATE: Virginia COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09335697B
Patent No. 6200804
GENEAL INFORMATION:
APPLICANT: BRAMS, Peter
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE, DOCKET NUMBER: 012712-150
FELECHONE, (703) 836-6620
FELECHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                               CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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CORRESPONDENCE ADDRESS:
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US-09-335-697B-17
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APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: WALSH, Edward E.
APPLICANT: WEWMAN, Roland Anthony
TITLE OF INVENTION: MOUTEALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERRAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1031 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCATGGAAAACCA 1090
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                                                                                   674 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAAGCAG
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US-09-335-697B-17
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COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,697B
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/770,057
FILING DATE:
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Search completed: April 6, 2003, 06:26:28 Job time : 67.1566 secs

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
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## ALIGNMENTS

Monoclonal antibody, cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematicsus; rheumatoid arthritis; psoriasis; type 1 diabetes mallitus; graft versus host disease; hetero-hybridoma; transfectoma. Primatised anti-human B7.1 antigen antibody 16C10 heavy chain Brams P, Hanna N, Shestowsky WS; AAW01822 standard; Protein; 476 AA 95US-0487550. 96WO-US10053 cynomolgus; 25-MAY-1997 (first entry) IDEC-) IDEC PHARM CORP Chimeric Macaca cynomo Chimeric Homo sapiens WPI; 1997-108638/10. Anderson DR, 06-JUN-1996; 07-JUN-1995; WO9640878-A1 19-DEC-1996, AAW01822; RESULT 1 AAW01822 

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Macaca fascicularis.
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                                                                             2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human BT.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
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                      monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaque primatized 16C10 heavy chain protein.
                                                            Claim 14; Fig 10B; 81pp; English
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  N-PSDB; AAT62513
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This sequence represents a primatized form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new concolonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such CC T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpure, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpure, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpure, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpure, systemic lupus erythematosus, theumatory bowel disease, allergy and multiple sclerosis, graft vs. Inflammatory disease and tumours. Optionally the deficiency virus) or inflammatory disease and tumours. Optionally the deficiency virus or inflammatory disease and tumours. Optionally the also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAb's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD2 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and entigen-specific immunoglobulin G (IgG) responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAP
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100.0%; Pred. No. 6e-149;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                              Hanna
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                                                                                                                              97WO-US19906
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Best Local Similarity 100.
Matches 476; Conservative
                                                                                                                                                                                                                                                             (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                              Anderson DR, Brams P,
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WO9819706-A1.
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476 AA;

Sequence

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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as cell cancer. Jymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell laukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vershost disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. cropin's disease and ulcerative colitis, food-related allergies e.g. migraine, rhintis and eczema, and other types of allergies. The present protein used in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2).
                                                                                                                                                                                                                                                                                                Protein sequence of primatised form of the heavy chain of 16C10 antibody.
                                                                                                                                                                                                                                                                                                                                     Human; macaque monkey; light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; mutein.
            420
                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
361 IEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNY
                  476
                                                                                        KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                          AAU11646 standard; Protein; 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Fig 5b; 89pp; English.
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                                                                                                                                                                                                                                                                   (first entry)
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Chimeric - Macac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                               PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNOFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                              300
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                       Gaps
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                                                    61 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR
                                                                                                                       LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                     EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
                                                                                                                                                                               Human; immune system associated protein; HISAP-4; immune disorder; infection; autoimmune disease; cancer.
                                        1 MKHLWFFLLLUVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
                                                                                                                                                                                                                                                                                           IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                       DKKABPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
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    Length 476;
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     . 6e-149;
. ac-149;
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  DB 23;
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                     0; Mismatches
100.0%; Score 2549;
100.0%; Pred. No. 66
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                      Conservative
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N-PSDB; AAC66522.
          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1998;
           Best Local Sim:
Matches 476;
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  Query Match
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19-DEC-1996
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                                                     number of human immune system associated proteins (HISAPS). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and call proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, Crohn's disease, irritable bowel syndrome, multiple solerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, soleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
                                           ces for a
These can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298
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                                                                                                                                                                                                                                                                                                                                                                                               120 RLFSVVGMVYNNW-FDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 KVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 355
                                                                                                                                                                                                                                                                                                                                   60 PPGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 APIEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPEN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 APIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPEN 415
                                                                                                                                                                                                                                            7; Gaps
                                                                                                                                                                                                                                                                       1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSI-SGGYGWGRNTRQ 59
                                                                                                                                                                                                                                                                                         1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSITSGGYYWSWIRQ 60
                                             sequences for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                          Query Match 91.9%; Score 2342.5; DB 22; Length 473; Best Local Similarity 93.3%; Pred. No. 3e-136; Matches 446; Conservative 9; Mismatches 16; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.
                                           present invention provides the coding and protein
              Claim 1; Column 53-56; 54pp; English
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Chimeric Homo sapiens.
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                                                                                                                                                                                473 AA;
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2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes (see also AATG2509 and AATG2510) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
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                                                                                                                                                                                                     Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-hoat di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.6%; Score 2309; DB 18; Length 476; 91.2%; Pred. No. 3.5e-134; ive 9; Mismatches 33; Indels 0;
                                                              Shestowsky WS
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                                                           Anderson DR, Brams P, Hanna N,
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                                                                                                                                                                                                                                                                                                           Claim 6; Fig 8B; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and graft-versus-host disease.
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Matches 434; Conservative
(IDEC-) IDEC PHARM CORP
                                                                                                                      WPI; 1997-108638/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              476 AA;
                                                                                                                                                       N-PSDB; AAT62510
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AAW63761
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This sequence represents a primatized form of the antibody 7C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibite binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple selerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD so no conjugated to a drug or coxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and inhibits antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppress.
                                                                                                                          Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
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Pred. No. 3.5e-134;
9; Mismatches 33; Indels 0;
                                                                                   Macaque primatized 7C10 heavy chain DNA.
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                                         (first entry)
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Best Local Similarity 91.2*
Matches 434; Conservative
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                                                                                                                                                                                                                                                            Macaca fascicularis.
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                                            29-SEP-1998
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AAW63761;
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Protein sequence of primatised form of the heavy chain of 7C10 antibody.
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                                                                            300
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                                                                                                                                                                                   361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVBWESNGQPENNY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                        361 IEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriacis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis
                       181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
                                                                                                    241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                         301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                            241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU11539 standard; Protein; 476 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2001; 2001WO-US16364.
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Chimeric - Macaca sp.
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or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive alivable disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 7C10, a primatised antibody used in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2).
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61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                   1 MKHLWFFILLVAAPRWVLSQVKLQQWGEGILQPSETLSRTCVVSGGSÍSGYYYWTWIRQT 60
                                                                                                                                                                                                                                                                                                                                  1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymerase chain reaction; primer; amplify; PCR; light chain; MAb; 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 IEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
                                                                                                                                                                                                                                                      Score 2309; DB 23; Length 476;
Pred. No. 3.5e-134;
9; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Mature heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Signal peptide"
20..475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR93553 standard; Protein; 475 AA
                                                                                                                                                                                                                                                        90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                             Matches 434; Conservative
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                   476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP08038178-A.
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The sequences given in AAR93553-54 represent the heavy and light chains respectively of a monoclonal antibody against a 65 kD antigen of human cytomegalovirus (hCWV). The DNA's encoding these sequences were amplified using the sequences given in AAT18040-58. The monoclonal antibody may be used in the diagnosis of hCWV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PPGKGLEWIGTIY-YSGSTYYNPSLKSRVTISVDASNNQFSLKLSSVTAADTAVYYCART 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP-QYYDLLTGSFPSYWGGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSIS-GGYGWGWIRQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKHLWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLTCTVSGDSISRSSYSWGCIRQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKTTPPVLDSDGSFFLYSKLIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                     Human monoclonal antibody binds to cytomegalovirus 65 kD antigen produced by primer amplification, used in the diagnosis of hCMV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.1%; Score 2296.5; DB 17; Length 475; Best Local Similarity 91.6%; Pred. No. 2e-133; Matches 437; Conservative 10; Mismatches 27; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system molecule, ISMO-2.
                                                                                                                                                                                                                                                                               Claim 4; Page 16-18; 22pp; Japanese
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                                 95JP-0030742
                                                                  94JP-0021628
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                                                                                                    (NISN ) NISSHINBO IND INC
                                                                                                                                                        WPI; 1996-154852/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 475 AA;
                                                                                                                      (TANA/) TANAKA H.
                                                                                                                                                                         N-PSDB; AAT18059
                                 20-FEB-1995;
                                                                  18-FEB-1994;
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Immune system molecules used in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation
                                                                                           The present sequence is an immune system molecule, ISMO-2 from an Incyte clone 2849752 isolated from the human breast tumour cDNA library (BRSTYUT13). This sequence is expressed in several libraries, generally those associated with cancer, cell proliferation, immune response or trauma. It shows homology to vertebrate immunoglobulin gamma heavy-chain. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain; variable region; insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                                                                                                                                  PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                                                                                                                                                                                EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPUTUSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGSISGGYGMGWIRQP
                                                                                                                                                                                                                                                                                                                 121 LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.4%; Score 2278; DB 21; Length 470; Best Local Similarity 91.4%; Pred. No. 2.7e-132; Matches 435; Conservative 9; Mismatches 26; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-rhesus D recombinant antibody D7C2 heavy chain.
                                                                   Claim 1; Pages 60-61; 69pp; English.
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AAR93166
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treatment; prevention; cell proliferation; immune system disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160..225
/note= "shows similarity to Ig superfamily protein
domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383...450
/note= "shows similarity to Ig superfamily protein
domain"
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                                                                                                                                                                                                                  note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                  note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                             note= "Protein kinase C phosphorylation site"
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                                                                            1..19
/label= Signal_peptide
                                                                                                                                         note= "N-glycosylated"
                                                                                                                                                                  "N-glycosylated"
                                                                                                    20..470
/label= Mature_ISMO-2
                                                                .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Corley NC,
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34..116
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N-PSDB; AAZ50012.
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                                       Homo sapiens
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Baughn MR;
                                                                           Peptide
                                                                                                    Protein
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Gaps

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The sequence is that of the reshaped CD4 antibody heavy chain CD4VHNEW-Ser30. Reshaped CD4 antibody can be used to induce tolerance against an antigen. It can also be used to alleviate autoimmune diseases such as rheumatoid arthritis, and to prevent graft rejection. Tolerance to a graft, e.g. an organ graft or a bone marrow transplantation can also be useful to alleviate allergies. Tolerance to allergens could also be achieved. See also AAR22753-R22763.
                     9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW 67
                                                                                                                                                                                                                                                                                                                            Antigen; CDR; complementarity determining region; graft rejection; autoimmune diseases; rheumatoid arthritis; allergy.
368 AKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

84.8%; Score 2162.5; DB 13; Length 467;

Best Local Similarity 87.6%; Pred. No. 3.4e-125;

Matches 411; Conservative 18; Mismatches 31; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation of framework-encoding regions of DNA encoding variable domain of rat or mouse antibody chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Complementarity determining region 2"
118..126
/note= "Complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanisation of antibodies binding to human CD4 antigen -
                                                                                           DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                       DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                             Reshaped CD4 antibody heavy chain CD4VHNEW-Ser30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waldmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "mature peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7; 74pp; English.
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                                                                                                                                                                                             AAR22759 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ23581
                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
                                                          peptide sequence encoded by
                                                                                                           /labels heavy_chain
/note= "human gamma 1 chain constant region
and the variable region from anti-rhesus D
antibody D7C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LFLVATATGVHSQVQLQQWGAGLLKPSETLSLTCTVYGGSFS-GYYWSWIRQPPGKGLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 VYNNWFDVWGPGVLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSGALTSGVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                        Margaritte C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%; Score 2217; DB 17;
90.4%; Pred. No. 1.6e-128;
iive 9; Mismatches 32;
                                                            mouse WH signal present synthetic linker"
                              1..19
/label= signal_peptide
/note= "mouse VH signal
                                                                                                                                                                                                                                                                                                                                                                                        Kaczorek M,
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          .ocation/Qualifiers
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(PROT-) PROTEINE PERFORMANCE
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Rattus rattus.
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                                                                 : : ...--WGQGSLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 178
                            187
                                                                                           NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
                                                                                                        NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK 238
                                                                                                                              SCDKTH7CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 307
                                                                                                                                                                     VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 367
                                                                                                                                                                               VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 358
                                                                                                                                                                                                         AKGOPREPOVYTLPPSKDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL 427
                                                                                                                                                                                                                           AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 418
                  IGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVVGM 127
LFNVATATGVHSQVQLQESGPGLVRPSQTLSLTCTVSGFTFS-NYGMAWVRQPPGRGLEW 66
                                                      128 VYNNWFDVMGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
                                                                                                                                           SCDXTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region 3"
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                                                                                                                                                                                                                                                         DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
                                                                                                                                                                                                                                                                                                                                                                                        Antigen, CDR, complementarity determining region, graft autoimmune diseases, rheumatoid arthritis, allergy.
                                                                                                                                                                                                                                               DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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/note= "Complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                      antibody heavy chain CD4VHNEW-Thr30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20..467
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N-PSDB; AAQ23571.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus
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The sequence is that of the reshaped CD4 antibody heavy chain CD4VHNAW-Thr30. Reshaped CD4 antibody can be used to induce tolerance against an antigen. It can also be used to alleviate autoimmune diseases such as rheumatoid arthritis, and to prevent graft rejection. Tolerance to a graft, e.g. an organ graft or a bone marrow transplantation can also be useful to alleviate allergies. Tolerance to also be useful to alleviate allergies. Tolerance to allergens could also be achieved. See also ARR22753-R22763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 IGSFYSSSGNIYYNPSLKSQVIISTDISKNQFSLKLNSMIAADIAVYYCVRDRLFSVVGM 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 VYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LFLVATATGYHSQVQLQESGPGLVRPSQTLSLTCTVSGFTFT-NYGMAWVRQPPGRGLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKVDKKVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCDKTHTCPPCPAPELLGGPSVPLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
Humanisation of antibodies binding to human CD4 antigen - by mutation of framework-encoding regions of DNA encoding variable domain of rat or mouse antibody chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; CDR; complementarity determining region; autoimmune diseases; rheumatoid arthritis; allergy
                                                                                                                                                                                                                                                                                                                                                                                   ; Score 2159.5; DB 1; Pred. No. 5.3e-125; 19; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reshaped CAMPATH-1 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
50..54
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                                                                                                Disclosure, Fig 6; 74pp; English
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.4%;
Matches 410; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR22757 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                      467 AA;
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Misc-difference
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                                                                                                                                                                                                                                                                                   WO9709351-A1
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Matches 409;
                                                                                        18-OCT-1997
                                                                                                                                                                                                                                                                                                          13-MAR-1997
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                                                                 AAW14927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                      RESULT 14
                               AAW14927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 GMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 -----FDYWGQGSLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 IGSFYSSSG--NTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDRLFSVV 125
                                                                                                                                                                                                                                                                                                                              Reshaped CD4 antibody can be used to induce tolerance against an antigen. It can also be used to alleviate autoimmune diseases such as rheumatoid arthritis, and to prevent graft rejection. Tolerance to a graft, e.g. an organ graft or a bone marrow transplantation can also be useful to alleviate allergies. Tolerance to allergens could also be achieved. See also AAR22754-R22763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LFLVATATGVHSQVQLEESGPGLVRPSQTLSLTCTVSGFTFTDFY-MWVRQPPGRGLEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEW 67
                                                                                                                                                                                                                                                                                                                    The sequence is that of the reshaped CAMPATH-1 heavy chain antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
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                                                                                                                                                                                                                                                 Humanisation of antibodies binding to human CD4 antigen - by mutation of framework-encoding regions of DNA encoding variable domain of rat or mouse antibody chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels 10;
          'note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

84.3%; Score 2148; DB 13;
Best Local Similarity 87.3%; Pred. No. 2.7e-124;
Matches 411; Conservative 16; Mismatches 34;
                                                                                                                                                                                            Gorman S D, Waldmann
                               /note= "signal peptide"
                                                      /note= "mature peptide"
                                                                                                                                                                                                                                                                                               Disclosure, Fig 5; 74pp; English
                                                                                                                           91WO-GB01578
                                                                                                                                               90GB-0020282
                                                                                                                                                                                            Clark M R, Cobbold S P,
 101..110
                                            20..470
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N-PSDB; AAQ23570.
                                                                                                                                                                    (GORM/) GORMAN S D.
                                                                                                                                                                                                                                                                                                                                                                                                              470 AA;
                                                                                                                         16-SEP-1991;
                                                                            WO9205274-A
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                      Peptide
                                            Peptide
 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 Polypeptides (AAW14925-27) respectively comprise the heavy chain regions of human gamma-4, gamma-4E carrying an L236E mutation in the hinge region, and gamma-4PE carrying L236E and $229P mutations. They can be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human 1964 Fc binding domain framework is combined with the antigen binding domains (GE9 1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune
                                                                                                                                                                                                                                                                CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma 4PE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, esp. useful for treatment of autoimmune disease, e.g. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.2%; Score 2145.5; DB 10
85.9%; Pred. No. 3.8e-124;
ive 19; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "site of S229P mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "site of L236E mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 91-93; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
248
AAW14927 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanna N, Newman RA, Reff ME;
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                                                                                                                                                                                                    Human gamma-4PE heavy chain.
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                                                                                                                                  (first entry)
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N-PSDB; AAT62870.
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PGKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCASNI 120
                            L-----KYLHWILYWGGGVLVIVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP 174
                                                                  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKV 234
                                                                                             DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                        EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                             EVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS 351
                                                                                                                                                                                          411
                                                                                                                                                                                                                                                                                                                                                        CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma;
                   LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                        EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY1CNVNHKPSNTKV
                                                                                                                                                                       IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                   transplant rejection; HIV; therapy; CE9 gamma 4
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                                                                                                                                                                                                                                                                                                                                       Human gamma-4 heavy chain.
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N-PSDB; AAT62868.
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3 Polypeptides (AAW14925-27) respectively comprise the heavy chain regions of human gamma-4, gamma-4E carrying an L236E mutation in the hinge region, and gamma-4PE carrying L236E and S229P mutations. They can be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IGG4 Fc binding domain framework is combined with the antigen binding domains (see also AAW14922-23) of macaque anti-

Claim 6; Page 82-84; 155pp; English.

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                                                                                                                                                                                                                                                                                                 PGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                                                                                                                                          61 PCKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLKSVTAADTAVYYCASNI 120
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human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. They can be used to treat autoimmune diseases such as rheumatoid arthritis.
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                                                                                                                                         18; Length
                                                                                                                                     84.1%; Score 2144.5; DB 18; Lengt
85.9%; Pred. No. 4.4e-124;
ive 19; Mismatches 39; Indels
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ne : 49.9575 secs
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                                                                                                    467 AA;
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Matches
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Sequence 9, Appli Sequence 10, Appl Sequence 51, Appl Sequence 51, Appl Sequence 901, App Sequence 742, App Sequence 6, Appli Sequence 931, App

Sequence 931, App Sequence 843, App Sequence 843, App Sequence 859, App Sequence 993, App Sequence 1021, Ap Sequence 1021, Ap Sequence 1131, Ap Sequence 1141, Ap Sequence 1142, Ap Sequence 1142, Ap Sequence 115, Ap Sequence 115, Ap Sequence 115, Ap Sequence 115, Ap Sequence 835, App Sequence 835, App Sequence 835, App Sequence 835, App

> US-09-935-868-14 US-09-796-692-836 US-09-796-692-982 US-09-796-692-991

10 US-09-291-299A-9 10 US-09-291-299A-10 9 US-09-928-115A-57 9 US-09-928-645-51 10 US-09-796-692-901 9 US-09-796-692-901 9 US-09-796-692-843 9 US-09-796-692-843 9 US-09-796-692-843 9 US-09-796-692-896 9 US-09-796-692-896 9 US-09-796-692-896 9 US-09-796-692-1011 9 US-09-796-692-1021 9 US-09-796-692-1021 9 US-09-796-692-1031 9 US-09-796-692-1041 9 US-09-796-692-1041 9 US-09-796-692-1041 9 US-09-796-692-1041 9 US-09-796-692-1041 9 US-09-796-692-1041

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VA
USA
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COUNTRY: US
ZIP: 22314
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Sequence 10, Appl Sequence 10, Appl Sequence 20, Appl Sequence 2, Appli Sequence 70, Appl Sequence 70, Appl Sequence 70, Appl Sequence 88, Appl Sequence 88, Appl Sequence 12, Appl Sequence 26, Appl Sequence 3, Appl Sequence 3, Appl Sequence 7, Appli
                                                                                          March 29, 2003, 09:14:52; Search time 9.04722 Seconds (without alignments) 1531.829 Million cell updates/sec
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                                                                                                                                                               1232
1 MRVPAQLLGLLLLWLPGARC......CQVTHEGSTVEKTVAPTECS 236
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/ cgn2_6/ptodata/1/pubpaa/USOB_NEW PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USOG_NEW PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USOG_NEW PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USOF_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/USO0_NEW PUB.pep:*
          GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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10 US-09-48-429B-10

10 US-09-747-669-6

9 US-10-001-857-202

9 US-10-01-857-202

9 US-10-124-905-2

10 US-09-863-161-70

10 US-09-852-797-70

10 US-09-852-797-70

10 US-09-852-797-88

10 US-09-853-161-88

11 US-09-853-161-88

12 US-09-853-161-88

13 US-09-853-161-88

14 US-09-853-161-88

15 US-09-853-161-88

16 US-09-853-161-88

17 US-09-853-161-88

18 US-09-853-161-88

19 US-09-853-161-88

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                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*
                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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RESULT 1

Sequence 10, Application US/10124905

TITLE OF INVENTION: WORKEY WONCELONIA ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRINATIZED FORMS THEREOF AS ITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRINATIZED FORMS THEREOF AS ITLE OF INVENTION: IMMUNOSUPERSANTS.

CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE
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Length 236;

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Query Match 100.0%; Score 1232; DB 9; Best Local Similarity 100.0%; Pred. No. 5.6e-52; Matches 236; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.9%
Matches 193; Conservative
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US-10-001-857-202
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LENGTH: 235
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "WONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                          61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                               61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                             FGGGTRLTVLGQPKAAPSVTLFPPSSEBLQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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                                                                                                                                                                                          1 MRVPAQLIGILILIMIPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
                                                                                                                                                                   1 MRVPAQLLGLLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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                                                                                             Length 236;
                                                                                                                                  Indels
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                              Score 1232; DB 9;
Pred. No. 5.6e-52;
                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/487,550
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-133
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Vo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 236 amino acids
                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 236; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-948-429B-10
                                     MOLECULE TYPE: protein US-10-124-905-10
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OPERATING SYSTEM:
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           amino acid
                               linear
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GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANTION: ANTIGEN BINDING FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
TITLE OF INVENTION: AND DETECTION OF CANCERS
TITLE REFERENCE: 31608201001
CURRENT APPLICATION NUMBER: US/09/747,669
PRIOR PRILING DATE: 2002-04-08
PRIOR PLING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FRAGSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
                                                                                                                                                             61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                            61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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  Gaps
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                                                     9
                                                                                       1 MRVPAQLIGILLILMILPGARCESVLIQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                        1 MRVPAQLLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                                                                                                                                                                                                                                                                                                                                                                                 AGVETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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83.9%; Pred. No. 2.5e-41;
iive 14; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Synthetic construct US-09-747-669-6
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Sequence 2, Application US/09948429B

Patent No. US20020177689A1

GENERAL INFORMATION:

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS

TITLE OF INVENTION: INMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AGVETITIPSKOSNNKYAASSYLSLIPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 236
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.0%; Score 973; DB 9; Length 234; Best Local Similarity 80.1%; Pred. No. 8.9e-40; Matches 189; Conservative 13; Mismatches 32; Indels
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APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGEN: INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   012712-131
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                               TELEPHONE: 703-836-6620
TELEBRAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 23 a maino acids TYPE: amino acids TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-10-124-905-2
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APPLICATION NUMBER:
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                        APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT APPLICATION NUMBER: 60/252,054
PRIOR PLING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
WUMBER OF SED ID NOS: 208
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10124905
Sequence 2, Application US/10124905
Barein No. US2010613641
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS THERE OF INVENTION: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTTPSKQSNN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 RPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 GARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYD-LHWYQQLPGTAPKLLIYDINK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 81.1%; Score 999.5; DB 9; Length 221; Best Local Similarity 87.4%; Pred. No. 4.8e-41; Matches 194; Conservative 12; Mismatches 13; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 KYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 221
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRETT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Bapien
US-10-001-857-202
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LENGTH: 221
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US-09-852-797-70
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APPLICANT: Stadler, Beda
APPLICANT: Vogel, Monique
TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST
TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO
TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR
TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR
CURRENT APPLICATION NUMBER: US/09/974,449
CURRENT FILING DATE: 2001-10-10
PRIOR PILICATION NUMBER: PCT/FP00/03288
PRIOR PILING DATE: 2000-04-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                                                                                                                                                                                                                                                                                                                              61 PGTAPKILIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                 1 MRVPAQLIGILILMILPGARCAYELTQPPSVSVSPGQTARITGGGDNSR--NEYVHWYQQK 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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83.1%; Pred. No. 9.7e-39;
Live 16; Mismatches 18; Indels 3;
                                                                                                                                                                                                Query Match 79.0%; Score 973; DB 9; Length 234; Best Local Similarity 80.1%; Pred. No. 8.9e-40; Matches 189; Conservative 13; Mismatches 32; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 38, Application US/09974449 ; Patent No. US20020141989A1
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acids
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Matches 182; Conservative
                                                                                                                              , MOLECULE TYPE: protein
US-09-948-429B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                linear
                                                                                                            TOPOLOGY:
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66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LILLILILTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP
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Sequence 70, Application US/09852797
Patent No. US20020172994A1
GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 70, Application US/09853161
Patent No. US20020076756A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TILE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P3
                                                                                                                                                                                   THE REPERBUCE: P2003P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR PELICATION NUMBER: 00/56,583
PRIOR PELICATION NUMBER: 00/152,060
PRIOR APPLICATION NUMBER: 00/152,060
PRIOR APPLICATION NUMBER: 00/152,060
PRIOR PILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 00/040,762
PRIOR PILING DATE: 1998-03-14
PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-03-16
PRIOR PELING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR PELING DATE: 1997-05-30
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65 KLLSYRNNNRPSGISERLSASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWMFGGGT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.8%; Score 885; DB 10; Length 235; Best Local Similarity 77.1%; Pred. No. 1.2e-35; Matches 178; Conservative 11; Mismatches 38; Indels 4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LILITILITHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP 64
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; Patent No. US20020125994a1
; APPLICANT: Rosen et al.
; TITLE OF INVENTATION: 28 Human Secreted Proteins
; TITLE OF INVENTATION: 28 Human Secreted Proteins
; TITLE OF INVENTATION: 2001-05-17
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT APPLICATION NUMBER: 06/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR FILING DATE: 1998-09-11
; PRIOR FILING DATE: 1998-09-11
; PRIOR FILING DATE: 1997-03-14
; PRIOR PLICATION NUMBER: 60/040,762
; PRIOR PLICATION NUMBER: 60/040,710
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR APPLICATION NUMBER: 60/040,100
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR PRILING DATE: 1997-05-30
; PRIOR PLING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
                   PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR PAPLICATION NUMBER: 60/048,100
PRIOR PRIOR DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR PILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PRIOR DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PELING DATE: 1997-12-19
SOFTWARE: PREDEITIN VOE: 2.0
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CORGANISM: Homo sapiens
US-09-852-659A-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LLLITLITHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQFP 64
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Sequence 70, Application US/09852659A

Fatent No. US2002007287A1

GENERAL INFORMATION:

TITLE OF INVENTYON: 28 Human Secreted Proteins

TITLE OF INVENTYON: 28 Human Secreted Proteins

TITLE OF INVENTYON: 28 Human Secreted Proteins

CURRENT APPLICATION NUMBER: US/09/852,659A

CURRENT FILING DATE: 2001-05-11

FRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 1998-09-11

FRIOR APPLICATION NUMBER: 09/152,060

PRIOR FILING DATE: 1998-09-11

FRIOR APPLICATION NUMBER: 1998-09-11

FRIOR APPLICATION NUMBER: 1998-09-11

FRIOR APPLICATION NUMBER: 1998-09-11

FRIOR APPLICATION NUMBER: 1998-09-11

FRIOR FILING DATE: 1998-09-11
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR APPLICATION NUMBER: 60/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR PRILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-03-12
PRIOR PELING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-19
PRIOR PELING DATE: 1997-03-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-06-05
PRIOR PELING DATE: 1997-06-05
PRIOR PELING DATE: 1997-06-05
PRIOR PELING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,309
PRIOR PELING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,309
PRIOR PELING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,309
PRIOR PELING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,306
PRIOR PELING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,306
PRIOR PELING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,306
PRIOR PELING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
PRIOR PELING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
PRIOR PELING DATE: 1997-12-19
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ORGANISM: Homo sapiens
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66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
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                                                                                                                                                                                                                                                                                                                         10 LLLLWLPGARCESV----LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP 65
                                                                                                                                                                                                                                                                                                                                                                                                5 LLLLTLLTHSAVSVVQAGLTOPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.6%; Score 882; DB 10; Length 235; Best Local Similarity 76.6%; Pred. No. 1.7e-35; Matches 177; Conservative 12; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ROBERLA INFORMATION: 5 Human Secreted Proteins TILLE OF INVENTION: 28 Human Secreted Proteins FILE OF INVENTION: 28 Human Secreted Proteins FILE OF INVENTION: 28 Human Secreted Proteins FILE OF INVENTION NUMBER: US/09/852,659A CURRENT FILING DATE: 2001-05-13 PRIOR FILING DATE: 2001-05-02 PRIOR FILING DATE: 1998-09-11 PRIOR FILING DATE: 1998-09-11 PRIOR FILING DATE: 1998-09-11 PRIOR FILING DATE: 1998-09-11 PRIOR FILING DATE: 1997-03-14 PRIOR FILING DATE: 1997-03-14 PRIOR FILING DATE: 1997-03-14 PRIOR FILING DATE: 1997-05-30 PRIOR PRIOR FILING DATE: 1997-05-30 
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        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-88
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
71.6%; Score 882; DB 9; Length 235;
Best Local Similarity 76.6%; Pred. No. 1.7e-35;
Matches 177; Conservative 12; Mismatches 38; Indels 4; Gaps
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Patent No. US20020076756A1

Patent No. US20020076756A1

APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

ITILE OF INVENTION: 28 Human Secreted Proteins FILE OF INVENTION: 28 Human Secreted Proteins FILE OF INVENTION NUMBER: US/09/853,161

CURRENT APPLICATION NUMBER: US/09/853,161

PRIOR APPLICATION NUMBER: 00/162,583

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR APPLICATION NUMBER: 60/040,702

PRIOR APPLICATION NUMBER: 60/040,100

PRIOR FILING DATE: 1997-05-30

PRIOR PILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,100

PRIOR PILING DATE: 1997-05-30

PRIOR PILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,357

PRIOR PILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,357

PRIOR PILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/057,755

PRIOR PILING DATE: 1997-05-30

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PRIOR APPLICATION NUMBER: 60/057,765
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFWHARE: PATENTIN Ver. 2.0
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-852-797-88
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ORGANISM:
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Search completed: March 29, 2003, 09:38:43
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LOCATION: (59)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (121)
.; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-225-301-1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                           119 STDSSSYYRVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTV 178
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                                                                126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
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5 LLELTLLTHSAVSVVQAGLTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPP 64
                                                                                                                                                                                           APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAlo6
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                       ; Sequence 1424, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
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239 APTECS 244
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RESULT 15

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APPLICANT: Heaks Corporation
APPLICANT: Heaks Corporation
APPLICANT: Hockal Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
FILE REPRENCE: AL-1
CURRENT APPLICATION NUMBER: US/09/828,995B
CURRENT PILING DATE: 2001-04-09
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR FILING DATE: 2000-04-07
SUGTWARE: PALENTH: 2000-04-07
SEQ ID NO 26
LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (147)
OTHER INFORMATION: The 'Xaa' at location 147 stands for Thr, Ala, Pro, or Ser.
NAME/KEY: misc_feature
LOCATION: (148)
OTHER INFORMATION: The 'Xaa' at location 148 stands for Ser, or Phe.
NAME/KEY: misc_feature
LOCATION: (149)
OTHER INFORMATION: The 'Xaa' at location 149 stands for Ser, or Phe.
LOCATION: (169)
OTHER INFORMATION: The 'Xaa' at location 169 stands for Ser, or Asn.
US-09-828-995B-26

C7 n* Score 826; DB 9; Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LILTLLAHCTGSWAQAVLNQPASVSGALGQKVTISCSGDTNDIDIFGVNWYQQLPGKAPT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.0%; Score 826; DB 9; Length 239; Best Local Similarity 70.0%; Pred. No. 7.6e-33; Matches 161; Conservative 21; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 TPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 KPSKQSNNKYAASSYLSLTPDKWKSHSSFSCLVTHEGSPVEKKVAPAKCS 239
. Sequence 26, Application US/09828995B
; Patent No. US20020165135A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Canis familiaris
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Best Local Similarity 100.
Matches 236; Conservative
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MOLECULE TYPE: protein
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3Y: linear
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STATE: VA
COUNTRY: USA
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STREET: 6
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Best Local S
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                                                                                                                                                   March 29, 2003, 09:06:24 ; Search time 8.38523 Seconds
   (without alignments)
   828.100 Million cell updates/sec
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                                                                                                                                                                                                                                           US-09-758-173-10
1232
1 MRVPAQLIGLLIMLPGARC.......CQVTHEGSTVEKTVAPTECS 236
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(GgnZ 6/ptodata1/jaa/5A COMB.pep:*

(GgnZ 6/ptodata1/jaa/5B_COMB.pep:*

(GgnZ 6/ptodata1/jaa/6A_COMB.pep:*

(GgnZ 6/ptodata1/jaa/6B_COMB.pep:*

(GgnZ 6/ptodata1/jaa/6B_COMB.pep:*

(GgnZ 6/ptodata1/jaa/6B_COMB.pep:*

(GgnZ 6/ptodata1/jaa/backfles1.pep:*
                   GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-049-672A-7
US-09-049-672A-10
US-09-049-672A-12
US-09-049-672A-12
US-09-049-672A-12
US-09-152-060-70
US-09-152-060-88
US-09-152-060-88
US-08-051-88-11
US-08-07-146-22
US-08-07-146-22
US-08-07-146-22
US-08-07-146-22
US-08-08-092-9
US-08-422-091-9
US-08-422-091-9
US-08-422-093-9
US-08-422-093-9
US-08-422-093-9
US-08-422-093-9
US-08-157-101A-5
US-08-157-101A-
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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RESULT 1
US-08-487-550-10
Sequence 10, Application US/08487550
Sequence 10, Application US/08487550
Sequence 10, Application US/08487550
Sequence 10, Application US/08487550
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
UNUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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Sequence 35, A
Sequence 4, Ag
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Sequence 5, Ag
Sequence 5, Ag
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: 1BM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTWARE: PerentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,550

FILING DATE: 07-UN-1995

CLASSIFICATION: 435

ATTORNEY, AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 012712-131

TELEPHONE: 703-836-6620

TELEFRANION FOR SECIED NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 236 amino acids

TVOE
PCT-US95-08743-153
US-08-812-586-16
US-08-049-672A-6
PCT-US94-0759-4
US-09-079-029-11
US-07-690-192-2
US-09-025-769B-18
US-08-33-400-37
US-08-35-769B-18
US-08-487-550-6
US-08-46-981-3
US-08-646-981-3
US-08-646-981-3
US-08-74-63
US-08-74-63
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US-08-665-202-43
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                               66 KLLIYGSRNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGVVFGGGT 125
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                                                                                                                   126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PGTAPKILLYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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                                                                                                                                            181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                             186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                           186 TIPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPIECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 234;
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79.0%; Score 973; DB 3; Length 23
Best Local Similarity 80.1%; Pred. No. 7.9e-71;
Matches 189; Conservative 13; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: EL PER PC COMPATIBLE
COMPUTER: PATHON SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATHON TO DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/COMPUTION INFORMATION:
TELEPHONE: 770-86.6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                  US-08-487-550-2
; Sequence 2, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELETRAL 103-808-0042 TELETRAL 103-808-0042 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 234 amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-2
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STATE: VA
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STREET: 69
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61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                         61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                     121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                          121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AGVETTTPSKOSNNKYAASSYLSLTPEOWKSHRSYSCOVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                             181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ı,
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yu, Henry
APPLICANT: Yu, Henry
APPLICANT: Wo.Young, Janice
APPLICANT: Gorgler, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Bughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
COMPASSOONERS: 28
COMPASSOONERS: 28
ADDRESSOONERS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LBM.Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERO for Windows Version 2.0
CURRINT APPLICATION DATA:
RPPLICATION NUMBER: US/09/049,672A
FILLING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: HEREMITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFRENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHANE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09049672A
Patent No. 613541
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IMMEDIATE SOURCE;
; LIBRARY: ADRETUTOS
; CLONE: 2492122
US-09-049-672A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
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                                                                                                                                                                                                                                                                                                                            US-09-049-672A-7
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184 ETITPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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REGISTRATION NUMBER: 39,132
REPERENCE/DOCKET NUMBER: PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: HEREMITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 31/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                     US-09-049-672A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-049-672A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    αq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AQLIGLILIMIPGARCESVITOPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Gaps
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry, Y. Tom
APPLICANT: Yue, Henry, Ver, Hong, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.3%; Score 965; DB 4; Length 235; Best Local Similarity 80.3%; Pred. No. 3.5e-70; Matches 187; Conservative 19; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 943.04

ZIP: 943.04

COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette
COMPUTER: DISKett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0497 US
                                                                                                                                                                                              Sequence 10, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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STRANDEDNESS: sir
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                                                                                                                                  RESULT 4
US-09-049-672A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDBADYYCQSYDSSLNAQVFGGGTR 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLGLLLLMLPGARCESVLTOPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LLLALLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGTTSNIASNSVHWYQLVPGAAPK 65
                                                                                                                                                                             APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: O'C-1E', Neil C.
APPLICANT: Guegler, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTOR: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
STORESPEE: Incvte backers
STORESPEE: Incvte backers
Query Match 78.3%; Score 965; DB 4; Length 235; Best Local Similarity 80.0%; Pred. No. 3.5e-70; Matches 184; Conservative 20; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
COFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                Sequence 12, Application US/09049672A
Patent No. 6135941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 GIRLIVLGOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AQLIGILILMIPGARCESVITQPPSVSGAPGQKVTISCTGSTSNIGGYDL-HWYQQLPGT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ALLLILLLIQDIGSWAQSALIQPASVSGSPGQSITISCTGTNNDVGSYNLVSWYQQHPGK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.5%; Score 955; DB 2; Length 235; 79.8%; Pred. No. 2.2e-69; tive 18; Mismatches 27; Indels
                  186 TPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235
187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                US-08-378-939-12
Sequence 12, Application US/08378939
Sequence 12, Application US/08378939
Sequence 12, Application US/08378939
SEGUENCE IS ST 6561
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: ROTHWELL, FIGG, ERNST & KURZ
STREET: SSS THIRTEENTH ST. N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASETELATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REPERSNEC/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 79.81
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-378-939-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                            STATE: D. C. COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                    20004
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US-09-152-060-70
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; Sequence 70, Application US/09152060

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66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 KLLSYRNNNRPSGISERLSASRSGATSSLTITGLQPEDEADYXCAAYDSSLAVWMFGGGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LLLLWLPGARCESV----LTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIPSKOSNNKYAASSYLSLIPEQWKSHRSYSCOVTHEGSIVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE REFERENCE: PZ003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1999-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FLING DATE: 1997-03-14
TITLE OF INVENTALIAN:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PEOG3P1.US
CURRENT FILING DATE: 1998-09-12
EARLIER PILING DATE: 1998-03-12
EARLIER FILING DATE: 1998-03-12
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER PILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER PILING DATE: 1997-03-04
EARLIER FILING DATE: 1997-03-06
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-06-06
EARLIER REPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 88, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-09-152-060-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-09-152-060-88
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Matches 178;
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Gaps

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64 LVIYADSERPSGIPARFSGSNSGNTATLTISGVEAGDEADYYCQVWDSTADHWVFGGGTR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LLGLLLLUWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LIGILAHFIDSA-ASYELSOPRSVSPGQTAGFICGG--DNVGRKSVQWYQQKPQAPV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hallman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Gordley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OP INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                          DB 4; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233
                                                                                                                                                                                                                                                                                                                    Query Match
69.6%; Score 857.5; DB 4; Length 2
Best Local Similarity 74.8%; Pred. No. 1.4e-61;
Matches 172; Conservative 16; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: End Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
TELECHOMICATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/GOOKET NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
              TELECOMMUNICATION INFORMATION:
              TELEPHONE: 703-02.
TELEPHONE: 703-02.
TELEPHX: 703-03-2021
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 233 amino acids TYPE: amino acid TYPE: amino acid TYPE: amino acid
                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-523-894-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-523-894-6

Sequence 6, Application US/08523894

Sequence 10. 6136310

GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: VA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 TIPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.6%; Score 882; DB 4; Length 235; 76.6%; Pred. No. 1.6e-63; tive 12; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: VA

COUNTRY: USA

ZIP: 22314-3187

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,894

FILING DATE: 06-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: TESKIN RODIN L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-165
EARLIER FILING DATE: 1997-05-30
EARLIER PELLING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-06-30
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 88
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 76.6
Matches 177, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-152-060-88
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SGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSVTLFPPSLEELQANKATLEELQANKATLVCLISDFYPGAVTLAWKADGRPVKAGVETN 188
                                                                                                                                                                                                                                                                                                                                                             Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                16 GVHSDIELTQDPAVSVALGQTVRITCQG--DSLRTYYASWYQQKPGQAPVLVIYGKNNRP 73
                                                                                                                                                                                                                                                                                                                                                                                                                 17 GARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-751-359-22

Sequence 22, Application US/08751359

Fatent No. 6143529

GENERAL INFORMATION:

APPLICANT: Michael, Nancy M

APPLICANT: Accavitti, Marianne;

APPLICANT: Thompson, Craig B

TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                      Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 KPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTAEKTVAPAECS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
CITY: Texas
COUNTR: Texas
COUNTR: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/751,359
FILING DATE: COCCURENTLY Herewith
                                                                                                                                                                                                                                                                                                   Query Match 65.3%; Score 804.5; DB 4;
Best Local Similarity 70.9%; Pred. No. 2.6e-57;
Matches 163; Conservative 10; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: CONCURRENTLY Herewith CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 520/1D NO: 22:
TELECOMMUNICATION INFORMATION
                       TELEPHONE: 703-413-3000
TELEFAX: 703-413-220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 229 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-793-450-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-751-359-22
                                                                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 YDLHWYQQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 YDSSLNAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA 171
                                                                                                                                                                                                                                                                                                                                                                                       42; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSVPTMAMMMLLLGLLAYGSGVDSQTVVTQEPSFSVSPGGTVTLTCGLSSGSVSTSNYPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRVPAQLLGLLLLWL----PGARCESVLTQPPSVSGAPGQKVTISC----TGSTSNIGG 51
                                                                                                                                                                                                                                                                                                                             Query Match 67.9%; Score 836; DB 4; Length 240; Best Local Similarity 70.2%; Pred. No. 7.8e-60; Matches 172; Conservative 17; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: MACGARITTE, THE STEL
APPLICANT: CHABETHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03.48A*1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION WHERE: F 94/10566
FILING DATE: 02.5EP-1994
ATTORNAPATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-799-450-6
; Sequence 6, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION;
                 INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LNODNOTOB
CLONE: 3056213
US-09-049-672A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
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59 APVTVIYANTNRPSDIPSRFSGSKSGSTATLTITGVQADDEAVYYCGSADSSSTAGIFGA 118
                                                                                                             124 GTRLTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAG 182
                                                                                                                                   64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG 123
4 APLILAVLAHTSGSLVQAALTQPSSVSANPGETVKITCSGDRSYYG-----WYQQKAPGS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFANNI (15) 775 TELEFANNI (15) 397-9338 TELEFANNI (15) 397-938 TELEFANNI (15) 526 TENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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US-08-761-277A-51
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                                                                                                                             4 APLLLAVLAHTSGSLVQAALTQPSSVSANPGETVKITCSGDRSYYG-----WYQQKAPGS 58
                                                                                                     5 AQLIGILLIMIPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQ-LPGT 63
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                                                                                                                                                                                                                                                                                                                                                   51.5%; Score 634.5; DB 4; Length 229; 55.8%; Pred. No. 1e-43; Live 32; Mismatches 62; Indels 9
                           51.5%; Score 634.5; DB 4; Length 229; 55.8%; Pred. No. 1e-43; Live 32; Mismatches 62; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/08907146
Patent No. 6316600
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,359
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REPRENCE/DOCKET NUMBER: ARSB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 512/474-757
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 55.8%
Matches 130; Conservative
                                                                Matches 130; Conservative
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ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-907-146-22
                                                 Similarity
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US-08-907-146-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 60
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                                                     183 VETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTEC 235
                                                                                                                                                                                                                                                                                                                   Sequence 51, Application US/08761277A

Sequence 51, Application US/08761277A

Patent No. 5972334

GENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And TITLE OF ENGURENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
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California
COUNTRY:
California
COMPUTER
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COMPUTER
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MEDIUM TYPE:
CALIFORNIA
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CALIFORNIA
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MEDIUM TYPE:
APPLICATION NUMBER:
CLASSIFICATION:
MAMA:
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APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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100.0%; Pred. No. 1.1e-38;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 705-8410
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RESULT 15 US-08-422-101-9

S AQLIGILLIMIPGARCESVLTQPPSVSCAPGQKVTISCTGSTSNIGGYDLHWYQQ-LPGT 63

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Sequence 9, Application US/08422101
Patent No. 5739277
GENERAL INFORMATION:
APPLICANT: Brad Snedecor
ITILE OF INVENTION: Altered Polypeptides with Increased
ITILE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORMESPED SADDESS: ADDESSEE: Generated, Inc.
STRIE: California
COMPUTE: California
COMPUTE: Lab San Bruno Blvd
CITY: South San Francisco
STATE: California
COMPUTE: 5.25 inch, 360 Kb floppy disk
COMPUTE: Bath (Generated)
COMPUTE: Bath (Generated)
APPLICATION DATA: MS/08/422,101
FILING DATE: 14-ARR-1995
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 105/08/1422,101
FILING DATE: APPLICATION NUMBER: 932-3
FILING DATE: ATTONNER: 115/252-981
TELEPHONE: 15/522-981
TELEPHONE: 15/522-981
TELEPHONE: 15/522-981
TELEPHONE: 105 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: APPLICATION COMPUTE: Innear
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44.5%; Score 548; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e-37;
Matches 105; Conservative 0; Mismatches 0; Indels
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Gaps . 0

Search completed: March 29, 2003, 09:17:44 Job time : 9.38523 secs

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5, 2003, 18:12:24 ; Search time 392.719 Seconds (without alignments) 8205.894 Million cell updates/sec
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1 ATGAAACACCTGTGGTTCTT......CCCTGTCTCCGGGTAAATGA 1431
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                                                                                                                                                                                                                                                                                                                                                                                                                                 4370478
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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|:_/SIDS2/gcgdata/
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Maximum DB seq length: 200000000
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                                                                                                                                April
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115:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length DB ID	DB 18	1D AAT62513	Description Primatised anti-hu
7 6	1431		13	AAV35489	Macaque primatized
7	1211		7.7	AAS17247	DNA sequence of a
r (	1515.6		18	AAT62510	Primatised anti-hu
nv	1315.8		19	AAV35485	Macaque primatized
۰	1315.8		24	AAS17243	DNA segmence of a
7	1276.4		22	AAC66522	Human immine syste
<b>c</b> 0	1261.2		17	AAT18059	Monoclonal antibod
σ	1261		21		Human immine syste

Anti-rhealla D reco	1 4	gamma-4	Gamma	tide	Human anti-RSV mon	CDNA of the heavy	Human cDNA encodin						Lung cancer relate	Lung cancer relate	Antibody D heavy c	Traget plasmid Man	Encodes heavy chai	Plasmid Glambda-1B	Monoclonal antibod	Monoclonal antibod	Plasmid Glambda-1A	Macaque primatized	DNA secuence of a	Plasmid Hu19BHcpcd	Plasmid Hu19CHcpcd	Primatised anti-hu	Reshaped CD4 antib	CD4	Hu19	Human anti-HBs hea	Plasmid Hu19AHcpcd	Anti-IqE VH expres		Chimeric 4H6 anti-	Human cDNA encodin
AAT26889	AAT62868	AAT62870	AAT62869	AAH74680	AAT61241	AAK98701	AAS22593	AAA09695	AAC98220	AAT61279	ABK64550	ABL62673	ABL65479	ABL66294	AAQ35099	AAV61794	AAQ20066	AAC84208	AAX06951	AAX06952	AAC84206	AAV35487	AAS17245	AAV41429	AAV41431	AAT13847	AAQ23571	AAQ23581	AAV41432	AAQ49944	AAV41427	AAT15932	0	AAC91018	AAS22718
17	18	18	18	22	18	24	22	21	21	18	24	24	24	24	14	19	13	22	20	20	22	19	24	19	19	18	13	13	13	14	13	17	22	22	22
1418	1404	1404	1404	42	42	1430	1644	1507	1798	1428	1599	1599	1599	1599	1617	19035	1549	1442	1449	1449	ø	1437	1437	42	42	3	1458	1458	42	57	6284	55	43	1431	2912
85.6	82.5	82.3	82.2	80.4	79.4	79.2	79.2	79.2	79.2	78.5	78.5	78.5	78.5	78.5	78.4	78.3	78.2	78.2	78.1	78.1	78.0	77.7	77.7	77.6	77.6	77.6	77.6	77.6		•	٠		76.9	٠	76.9
1224.8	1181		1176.2	ä	1136.4	1134			1133.4	1123.6	1122.8	1122.8	1122.8	1122.8	1121.2	120	1119.6	1119	1118	1118	1115.8	1112.4	1112.4			1110.8		•	1109.2	1107.8	1102.8	N.	1101	110	1100.8
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	8	39	40	41	42	43	44	45
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## ALIGNMENTS

RESULT 1

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Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
                                                                                                         Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimtune disease; idlopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
                                                                                                                                                                                                                                                                                                                                                         Brams P, Hanna N, Shestowsky WS;
            AAT62513 standard; DNA; 1431 BP.
                                                                                                                                                                                                                                                                                   96WO-US10053.
                                                                                                                                                                                                                                                                                                          95US-0487550
                                                                                                                                                                                               Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                           Anderson DR,
                                                           25-MAY-1997
                                                                                                                                                                                                                                                                                 06-JUN-1996;
                                                                                                                                                                                                                                                                                                        07-JUN-1995;
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AAT62513
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1080 1080 1140 1200 1200 1260

1260

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Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
                                                                                              721 GACAAGAAAGCCGCGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGGGCA
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                                                                                                                                                                                                                                                                                                                                             2 DNA sequences (AAT62512 and AAT62513) respectively code for primatised forms (AAW01821 and AAW01822) of the light and heavy chains of cynomologus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes are inserted into an expression vector (pref. NBCSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAM01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
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useful for treating autoimmune disease or graft-versus-host disease
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100.0%; Pred. No. 8.5e-286;
ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                  Claim 11; Fig 10B; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and graft-versus-host disease.
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WPI; 1997-108638/10.
                                          P-PSDB; AAW01822
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New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
                                                                                                                           for treating diseases that involve Libracells, e.g. graft rejection or tumours
                                                                                                                                                Example 7; Fig 5b; 87pp; English
                                                                                       WPI; 1998-286601/25
                                                                                             P-PSDB; AAW63765
                                                                        Anderson DR,
WO9819706-A1
                             29-OCT-1997;
                                           08-NOV-1996;
               14-MAY-1998
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Hanna

Brams P,

PHARM

97WO-US19906 96US-0746361 This sequence encodes a primatized form of the antibody 16C10 heavy chain macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibite binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoinmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. tost diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumnours. Optionally the MAD be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppress.

Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;

ö GTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120 180 240 240 300 300 360 360 CTITITICAGIIGITGGAAIGGITIACAACAACIGGITCGAIGICIGGGGCCCGGGAGIC 420 9 9 1 Arganacaccristiscrictrictric recressive activities are a recreated and a rec AACCCCTCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC CCAGGGAAGGGGCTGGAGTTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 100.0%; Score 1431; DB 19; Length 1431; 100.0%; Pred. No. 8.5e-286; ive 0; Mismatches 0; Indels 0; ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCC Best Local Similarity 100. Matches 1431; Conservative 121 61 61 121 181 181 241 241 301 301 361 g g g ઠે ò ò ઠે 엄 ઠે 엄 셤 ઠે

RESULT 3 AAS17247

1020 1020 1080 1080 1200 1200 1260 480 480 540 540 600 600 099 999 720 720 780 780 840 840 900 900 960 CTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGAATGTCTGGGGCCCGGGAGTC 661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTG ATCGAGAAAAACCATCTCCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCCATCGGTCTTCCCCCTGGCACCCTCC TCCAAGAGCACCTCTGGGGGCACAGGGCCCTGGCCTGGTCAAGGACTACTTCCCC GACAAGAAGCCCACCAATCTTGTGAAAACTCACACACACGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 961 cadaAcadeAcAcAcAcAcAcAcGTAcCGTGTGGTCACCGTCCTCACCGTCCTGCACCAG TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCAGCCGGAGAACAACTAC AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 541 GAACCGGTGACGCTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGC AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACCCAAGGTG CCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTC 841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT 841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTGGTCGTGAGCCACGAGAAGACCCT GAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCG GAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCG GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCAGCCCCC ATCGAGAAAACCATCTCCAAAGCCCAAAGGCCCCCGAGAACCACAGGTGTACACCCTG CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGC AAGACCACGCCTCCCGTGCTGGACTCCGACGCTCCTTCTTCTTACAGCAAGCTCACACC CTGGTCACCGTCTCACCTAGCACCAAGGGCCCATCGGTCTTCCCCCCTGGCACCCTCC GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCGTGATGCATGAGGCT CTGCACACACCACTACACGCAGAAGACCTCTCCCTCTCTCCCGGTAAATGA 1431 421 421 481 541 661 721 1021 1081 1081 1141 1201 601 721 781 781 901 1021 1141 1201 1261 1261 1321 1321 901 961 1381 1381 ò ద à g ò g ò g ò 요 g ద g g ద g ò ò ò ò g a g 유 ò ò ò ò ò ò 셤 ò

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(first entry)

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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD86) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is concer where B cells promote the growth and/or metastasis of tumours, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autcoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-ver-host disease. The antibody is useful for immunosuppression or praft-ver-host disease. The antibody is useful for immunosuppression or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative collitis, food-related allergies e.g. Crohn's disease and ulcerative collitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the heavy chain of 16Cl0, a primatised antibody in interleukin-2 (IL-2).
                                                                                                        DNA sequence of a primatised form of the heavy chain of 16C10 antibody
                                                                                                                                         Human, macaque monkey, light chain, primatised antibody, 16C10 antibody neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen, CB6; B cell cancer, metastasis; tumour; B cell lymphoma; B cell leukaemia, autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                                                                                                                                                                                                      interleukin-2; IL-2; mutant; ds
AAS17247 standard; DNA; 1431 BP
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Chimeric - Macaca sp.
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P-PSDB; AAU11646.
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                                                                        12-MAR-2002
                                                                                                                                                                                                                                                                                                              Synthetic.
                                    AAS17247
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                                                                                                                                                                                                                                                                                                                                                   Key
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Brams

8; Fig 5b; 89pp; English

/product= "Heavy chain of 16C10 antibody"

Location/Qualifiers

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ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
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1 ATGAAACCCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCGTCTCCCAG
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100.0%; Score 1431; DB 24; Length 1431; 100.0%; Pred. No. 8.5e-286; ative 0; Mismatches 0; Indels 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DNA sequences (AAT62509 and AAT62510) respectively code for primatised forms (AAW01817 and AAW01818) of the light and heavy chains of cyromolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                  1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCTGACCTGCTGGTCAAAGGC 1200
                                                                                                                               1201 TICTATCCCAGCGACATCGCCGTGGAGGAGGAGCAATGGGCAGCCGGAGAAACAACTAC 1260
                                                                                                                                                                                                                                                               1081 ÀTCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
                                                                                                     TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCCAGCCGGAGAACAACTAC 1260
                                                                                                                                                                          AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTTCTTCCTCTACAGCAAGCTCACC 1320
                                                                                                                                                                                                                                             GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                            AAGACCACGCCTCCCGTGCTGGACTCCGACGCTCCTTCTTCTTCTTCTACAGCAAGCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody, cynomolgus monkey, macaque, 7C10, primatised antibody, B7 antigen, CD28, immunosuppressive, autoimmune disease, idiopathic thrombocytopaenia purpura; systemic lupus erythematosus, rheumatoid arthritis, psoriasis, type 1 diabetes mellitus, graft versus host disease; hetero-hybridoma, transfectoma, ss.
                                                                                                                                                                                                                                                                                                               CTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAATGA 1431
                                                                                                                                                                                                                                                                                                                                 1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primatised anti-human B7.1 antigen antibody 7C10 heavy chain
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Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;
                                                                                                                                  Pred. No. 4.8e-262;
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          961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
                                                                                                                                                                                        AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
                                                                                                                       1201 TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCGGCGGAGAACAACTAC
                                                 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGAAGCCCTCCCAGCCCCC
                                                                                      1081 ATCGAGAAACCATCTCCAAAGCCAAAGGCCACCCCGAGAACCACAGGTGTACACCCTG
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/product= 7C10 heavy chain
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from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunosuppression or small molecule immunosuppressants. Blocking B7/CD28 interactions or induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression and succines.
                                                                                                                                                                                                                                                         This sequence encodes a primatized form of the antibody 7C10 heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;
cells, e.g. graft rejection or tumours
                                                                                                                      Example 7; Fig 3b; 87pp; English
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961 CGGGAGGAGGAGTACAACAGCACGTACCGTGTGGTCCTCACCGTCCTGCACCAGC 1020
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                                                                                                                                                                                                                                                                                                                 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1140
AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACAAGGTG 720
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                                          GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACATGCCCACCGTGCCCAGCA
                                                                                        CCTGAACTCCTGGGGGACCGTCAGTCTTCCTTCCCCCCAAAACCCAAGGACACCCTC
                                                                                                    CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
                                                                                                                                   ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
                                                                                                                                               GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCG
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                                                                                                                                     Human; macaque monkey; light chain; primatised antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7 antigen; CD80; B7 2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-va-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
                                                                                                   DNA sequence of a primatised form of the heavy chain of 7C10 antibody.
                                                          12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                   Chimeric - Homo sapiens.
Chimeric - Macaca sp.
Synthetic.
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241 AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 300

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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating the seases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell lymphoma, as date to a diseases such as B cell sprombocycopenta purpura, systemic lupus, erythematcous, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, chinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the heavy chain of 7Cl0, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                      Location/Qualifiers
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The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPS). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atheroselerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
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94.7%; Pred. No. 6.4e-254;
tive 0; Mismatches 61; Indels 15;
                                                                                                                                                                                                       Human immune system associated protein HISAP-4 coding sequence
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              1381 CTGCACAACCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythematosus, arteriosclerosis, cirrhosis and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corley NC,
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                                                                                                           AAC66522 standard; cDNA; 1567
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Best Local Similarity 94.7
Matches 1358; Conservative
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P-PSDB; AAB36206
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65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAAGCATCTGTGGTTCTTCCTCCTGCTGGTGGCTCCCAGATGGGTCCTGTCCCAG 60
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88.1%; Score 1261.2; DB 17; Length 1431;

Best Local Similarity 93.9%; Pred. No. 8.6e-251;

Matches 1347; Conservative 0; Mismatches 78; Indels 9; C
1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
              1446 GCTCTGCACAACCACTACACAGAAGAGCCTCTCCCTGTCCCCGGGTAAATGA 1499
                                                                                                                                                                            Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
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1/.1429 a
1/.157
/*tag= b
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1426..1431
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                                                                                            AAT18059 standard; DNA; 1431
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Immune system molecules used in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation
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Gorgone G, Guegler KJ, Patterson C;
                                                                                                                                                                                 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTC
                                                                                                           <u> ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG</u>
                                                                                                                                                                                                                                                                  GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCCGGGTAAATGA 1428
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immunoglobulin gamma heavy-chain"
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/bound moiety= "Hybridisation probe"
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135.1487
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/product= "Mature ISMO-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system molecule, ISMO-2 cDNA.
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Baughn MR;
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                                                         DB 21; Length 1634;
The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with the immune system and
                                                                           Indels
                                      Sequence 1634 BP; 369 A; 541 C; 432 G; 292 T; 0 other;
                                                      Score 1261; DB 21;
Pred. No. 9.6e-251;
0; Mismatches 65;
                                                       Query Match
Best Local Similarity 94.2%;
Matches 1348; Conservative C
                   cell proliferation.
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Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; heavy chain; gamma 1; variable region; insect host cell; baculovirus; recombinant production;
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                                                                                                                                     721 GAGCCCAAATCTTGTGACAAACTCACACATGCCCACGGGGCCCAGCACCTGAACTCCTG
                                                                                                                                                                                                                                                                                                                   841 ACCCCTGAGGTCACATGCGTGGTGGTGGTGGAGCCACGAAGACCCTGAGGTCAAGGTCCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.6%; Score 1224.8; DB 17; Length 1418; Best Local Similarity 93.0%; Pred. No. 2.7e-243; Matches 1319; Conservative 0; Mismatches 87; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                                          The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence encodes a recombinant IgM-D7C2 heavy chain fused to a mouse VH signal peptide.
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                                                                                                                                                                            Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1418 BP; 333 A; 458 C; 378 G; 249 T; 0 other;
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                                                                  Kaczorek M,
                                                                                                                                                                                                                                                                   Claim 1; Page 35-37; 46pp; French
(INSP ) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE.
                                                                  Edelman L,
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CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
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                                                                                                                                                                                                                                                                                                                                                                            Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, esp. useful for treatment of autoimmune disease, e.g. rheumatoid
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0; Mismatches 112; Indels
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                                                                                          Homo sapiens
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                                                 241 AATCCCTCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCCC
                                                                                                                      CTGAAACTGAGGTCTGTGACGCCGCGGGCACGCCGTCTATTACTGTGCGAGTAATA--
                                                                                                                                                                                    GACAAGAGAGTTGAGTCCAAATATGG------TCCCCCATGCCCATCATGCCCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying the L236E mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IG4 Fc binding domain framework is combined with the antigen binding domains (see also AAW14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and climinate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                       CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma-4E; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
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90.2%; Pred. No. 2.8e-233;
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                             BP.
                                                                                                                            Human gamma-4E heavy chain DNA
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                             DNA; 1404
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Matches 1291; Conservative
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                                                                        1353
       GTGGACAAGAGCAGGTGGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity determining region; CDR; single chain antibody; ScFv; hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
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/*tag= a
/product= "single chain antibody"
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Pred. No. 4.5e-228;
0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of a single chain antibody
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similarly used. The transfected host cells provide a constant, stable supply of anti-RSV F-protein hMAbs for use in the treatment or prevention of RSV infection.
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Pred. No. 4.6e-225;
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                                                                                                                      1274 CCGTGCTGGACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1333
1271 CCGTGCTGGACTCCGACGGCTCCTTTCTTCTCTACAGCAAGCTCACGTGGACAAGAGCA 1330
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GGCACGAG(G). Size-selected >500bp for average insert size iskb. Library constructed by Ling Hong in the laboratory of Gerald Mn. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript IT RT (Life Technologies). Note: this is a NIH_MGC
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Pred. No. 4.2e-219;
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Matches 923; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
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SITH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs=r@mail.inh.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2466 row: m column: 16
High quality sequence start: 3
High quality sequence stop: 675.
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                                                                                                                                                                                   876 CAGAGCAGCAGCAGCAGCAGCAGCACTCTTCTCATGCTCCCGTGATGCATGAAGCTCTGCAC
                                  816 ACGCCTCNCGTGCACTCCGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGGA
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1267 ACGCCTCCCGTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACGTGGAC
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/lab_hote="hulb (phage-resistant)"
/lab_hote="hulb (phage-resistant)"
/note="Organ: spleen; Vector: poTB7; Site_1: Xhol; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Anol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Homg in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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     cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 01
Plate: LLCM2464 row: a column: 01
High quality sequence stop: 705.
Location/Qualifiers
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59.4%; Score 850.4; DB 14; Length 958;
Best Local Similarity 99.2%; Pred. No. 6e-206;
Matches 865; Conservative 0; Mismatches 6; Indels 1;
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AGENCOURT_8352177 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277512

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BQ706140

BS706140.1 GI:21845039
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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 958)
MTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                      AATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC
                                                                                       CGTCAGTCTTCCTCTTCCCCCAAAACCCAAGAAACCCTCATGATCTCCCGGACCCCTG
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Email: cgapbs.remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="INAGE:4852076"
/clone_lib="NIH MGC.48"
/tissue_type="primary B-cells from tonsils (cell line)"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="lung (phge-resistant)"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into BcoRIX/Nho! sites using the
following 5' adaptor: GGCA/GAG(G). Size-selected -550bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: Liss is a NIH MCC Library."
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Umpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: egapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLCM169; row: o column: 21

High quality sequence stop: 888.
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Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 926)
                                                                 1278 GCTGGACTCCGACGCCTCCTTCTTCCTCAAGCAAGCTCACCGTGGACAAGAGCAGGTG 1337
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 988)
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National Institutes of Health, Mammalian Gene Collection' (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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62 CTACTCCCTCAGCAGCGTGGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
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605 GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAA
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/db xref="taxon:9606"
/clone="INAGE:27561"
/clone lib="NHH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: poTB7; Site 1: Xho1; Site 2: ECRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zah-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrabed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
trow: c column: 02
High quality sequence stop: 716.
Location/Qualifiers
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| /organism="Homo sapiens" | /olone lib="NIH MGC 113" | /olone lib="NIH MGC 113" | /olone lib="NIH MGC 113" | /olone lib="Organ: spleen; Vector: poTB7; Site l: XhoI; Site 2: CCORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/AhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 901)

MIH-MOC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1939 row: j column: 20
High quality sequence stop: 834.
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1053 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
                                             665 GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAACCATCTCCCAAAGCCAAAAGGGCA
                                                                                                                                                                                         725 GCCCCGAGAAACACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAA-CA
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bp mRNA linear EST 02-APR-2002 Homo sapiens cDNA clone IMAGE:5924769

1029 bp AGENCOURT\_6876667 NIH\_MGC\_99 Ho 5', mRNA sequence. BQ063185 BQ063185.1 GI:19890681 EST

DEFINITION

ACCESSION

EST.

VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
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Email: cgapbs-r@mail.inh.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLCMMO95 row: g column: 10

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High quality sequence stop: 723.

Location/Qualifiers

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT_8353641 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279643
5', mRNA sequence.
BQ708022
BQ708022.1 GI:21846921
EST.
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                                                                                                                                                                            61 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGGTGACCGTGCCCTCCAGC 120
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                                                                                        1 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
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  Pred. No. 6.3e-199;
                      0; Mismatches
  97.68;
  Best Local Similarity 97.6
Matches 866; Conservative
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/db_xere="texton:9606"
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/clone="lib="NIH MGC_113"
/clone="lib="NIH MGC_113"
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887 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
5', mRNA sequence.
BQ711255
BQ711255.1 GI:21850154
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1 (bases 1 to 881)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                           CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAACCACAGGTGTACACCCTGCC 1142
                                                                                                                                                                                                                                                                                                CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAA 1262
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                                                                                                                                                                                                             CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: m column: 20
High quality sequence stop: 681.
                                                                                                                                                                                                                                                                                                                                                                                                                              843
484 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCCACCGTCCTGCACCAGGA 543
                                                               544 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCT
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                                                                                                                                                   604 CGAGAAAACCATCTCCAAAGCCAAAAGGGCACCCCGAGAAACCACACAGGTGTACACCCTGCC
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                                         CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCAT
                                                                                                                                                                                                                                                Score 822.8; DB 14; Length 887;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                         Email: cgapba-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2469 row: i column: 20
High quality sequence stop: 667.
Location/Qualifiers
ree
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 918)

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                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/db xref="taxno" septimes" /db xref="taxno" septimes" /db xref="taxno" septimes" /clone="lib="NIH MGC:13" /clone="lib="NIH MGC:13" /lab host="Dhl0B (phage-resistant)" /lab made by Oligo-dr priming. Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies). Note: this is a
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Bukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 995)
Math-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: 1 column: 16
High quality sequence stop: 718.
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                                         Score 818.6; DB 14; Length 995;
Pred. No. 7.9e-198;
0; Mismatches 34; Indels 2;
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Best Local Similarity 96.0%;
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BQ711291 AGENCOURT\_8347186 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6279096

RESULT 11 BQ711291 LOCUS DEFINITION

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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Clone='IMAGE:6279056"
/ Clone='IMAGE:6279056"
/ Clone='IMAGE:6279056"
/ Lab_host="DH10B (phage-resistant)"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2468 row: column: 01
High quality sequence stop: 721.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT 6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343 5', mRNA Fequence. BQ064886 BQ064886. BC1:19893932 EST.
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Low Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
Plate: LLCM2107 row: e column: 24

High quality sequence stop: 573.
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                                                                                                                                            1151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTACAGCAAGCTCACCGTGGACAAGAG 1331
                                                                                                                                                                                                                                                                           GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCCAG 1211
                                                                                                                                                                                                                                                                                                                                                                                                         CGACATCGCCGTGGAGTGGGAGAATGGGCAGCGGAGAACAACTACAAGACCACGCC 1271
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                                                                                                                                                                              CATCTCCAAAGCCAAAGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 540
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|clone=lib="NIH_MGC_99"
| Lissue_type="lymphoma, cell line"
|lab_hogt="DH10B (phage-resistant)"
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/organism="Homo sapiens"
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1371

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Divaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Inchases I to 940)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 619.

High quality sequence stop: 619.
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/lab_host="nh10B (phage-resista
                                                                                                                                                                                                                1193 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCAGCCGGAGA 1252
           670 ACAACTACNAGAACACCGCCCCCCGTGCACGACCGCCGCCTCCTTCCTCCTACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGAGGGTCTGGAC-ACCACTAACCGCAGAAGACCTCTTCCTGTCTCCCGGGAAATGA
                                                                                                                                   490 CAGCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
                                                                                                                                                                                                                                                      610 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAAGCAATGGGCAGCCGGAGA
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/organism="Homo sapiens"
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/clone="IMAGE:6301961"
/clone="IMAGE:6301961"
/clone="IMAGE:6301961"
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/lab host=="bulling (phage-resistant)"
/note="Corgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/AhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis ktt (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library.
31 a 306 c 245 g 152 t 2 others
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                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://image.lln.gov
Plate: LLCM2818 row: K column: 18
High quality sequence stop: 547.
                                                                                                               Homo gapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 936)
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                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                GI:21850626
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Matches 826;
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    Length 940;
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 Score 796; DB 14;
Pred. No. 4.5e-192;
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammália; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:627598"
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                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The Lim.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMA464 row: b column: 03
High quality sequence stop: 749.
Location/Coulifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 7.1e-190;
0; Mismatches 57; Indels 15;
                                                                                                                        Contact: Robert Strausberg, Ph.D.
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92.5%;
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Matches 886; Conservative
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.075 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1134
                                          AAAGGCTTCTATCCCAGCGACATC-GCCGTGGAGTGGGAGCAATGGGCAGCCGGAGAA 1253
                                                                                    CAACTACAAGACCACGCCTCCCGGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAA 1313
                                                                                                         TGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1431
                                                                                                                                      719
1015
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Search completed: April 6, 2003, 06:20:50 Job time : 2733.68 secs

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GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen_Ltd.
                  Copyright
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- protein search, using sw model OM protein

March 29, 2003, 09:06:24; Search time 10.5919 Seconds (without alignments) 2141.995 Million cell updates/sec Run on:

US-09-758-173-10

1 MRVPAQLLGLLLLWLPGARC.....CQVTHEGSTVEKTVAPTECS Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues

283224 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:\*
1: pir1:\*
3: pir2:\*
1: pir3:\*
: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

chain V chain -chain NI chain -chain NI chain -chain chain -chain NI chain chain V chain -chain (B chain lambda chain chain chain chain chain . Description lambda SUMMARIES \$25758 \$25756 JE0245 \$25748 \$25738 \$25731 \$25747 \$25751 \$69130 \$25753 S03401 S14675 B49444 S25759 S25749 JE0247 S25745 A42193 DB Query Match Length Score 1010.5 1000.5 1006 1006 1003.5 1001 989.5 987 986 967.5 Result

9 ' <del>⊼</del> , Z 236 235

186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 187 IPSKOSNNKYAASSYLSLIPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS

S25752 Ig lambda chain - human C;Species: Homo sapiens (man)

RESULT 2

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lambda	ig lambda chain - Ig lambda chain -	lambda	lambde	lambda	light	lambda	lambda	lambde	lambda	lambda	lambda	lambda	lambda	lambda
S25740	S70431	PT0220	S17399	S49449	A21177	PC4156	S12441	S12442	S12443	S12440	A39949	A39956	L2HU	823626
190 2	212 2	181 2	232 2	230 2	213 2	214 2	118 2	118 2	118 2	118 2	118 2	234 2	105 1	149 2
66.2	0.00 0.00	52.7	52.3	52.2	51.2	50.8	49.2	48.9	47.2	46.8	46.5	44.6	44.5	44.4
815	737.5	649.5	644.5	643	630.5	625.5	909	603	581	576	573	550	548	547.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of A;Reference number: S04601; MUID:89296497; PMID:2500644
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               126 LTVLGQPKAAPSVTLFPPSSEBLQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 235;
                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-130 < KLS2.
A; Cross-references: EMBL:X14583
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: hereroterramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-235/Product: Ig lambda chain #status predicted <MAT>
F;150-218/Domain: immunoglobulin homology <IMM>
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83.4%; Score 1027; DB 2;
Best Local Similarity 87.0%; Pred. No. 8.5e-60;
Matches 200; Conservative 12; Mismatches 18;
Ig lambda chain precursor - human
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C,Accession: S25757
R;Combridato, G; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25557
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
                                                                                                                                                                                                     Id lambda chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 329258
R;Chouchane, L.; van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Eur. J. Blochem. 207, 1115-1121, 1992
Bir. J. Blochem. 207, 1115-1121, 1992
A;Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PDRFSGSKSCTSASLAITGLQAEDEGDYYCQTYDISLTV-VFGGGTKLTVLGQPKAAPSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNÅ
A,Residues: 1-216 <GNO
A,Residues: 1-216 <GNO
A,Note: only part of the coding sequence is given
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: pyrcoglutemanic acid
F,131-199/Domain: immunoglobulin homology <IMM>
F,131-199/Domain: immunoglobulin homology <IMM>
F,11/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
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                                  186 TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
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83.0%; Pred. No. 1.9e-58;
iive 20; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.7%; Score 1006; DB 2; 89.9%; Pred. No. 1.8e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S29258
A;Status: preliminary
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Matches 195;
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: S25752 R;Combriato, G; Klobeck, H.G. R;Combriato, G; Klobeck, H.G. Bur. J. Ish3-1822, 1991 A;Title: V(lambda) and J(lambda) C(lambda) gene segments of the human immunoglobulin lamp A;Reference number: S16439; MUID:91257162; PMID:1904362 A;Accession: S2575 A;Accession: S2575 A;Status; preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-233 <COM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iglandda chain - human

(c)Species: Homo Sapiens (man)

(c)Species: Homo Sapiens (man)

(c)Species: Homo Sapiens

(c)Accession: $25746

R;Combriato, G:; Klobeck, H.G.

A;Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lam

A;Reference number: $16439; MUID:91257162; PMID:1904362

A;Accession: $25746

A;Accession: $25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                              PID:933734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTVLGOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPSKOSNNKYAASSYLSLTPEOWKSHRSYSCOVTHEGSTVEKTVAPTECS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; P:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.3%; Score 1014; DB 2;
84.8%; Pred. No. 5.8e-59;
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84.4%; Pred. No. 1e-58;
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
82.3%; Score 1014; D:
Best Local Similarity 84.8%; Pred. No. 5.8e
Matches 195; Conservative 15; Mismatches
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Best Local Similarity 84.4%
Matches 195; Conservative
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A.Accession: $21066
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-213 - DLO-
A.Residues: 1-213 - DLO-
A.Residues: 1-213 - DLO-
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin N region; immunoglobulin homology
C.Reywords: heterotetramer; immunoglobulin
F;128-196/Domain: immunoglobulin homology < MMA>
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Cispecies: Homo sapiens (man)
Cispecies: Alono sapiens (cispecies: Alono 26-May-1995 #text_change 21-Jan-2000
Cispecies: Alono 22-742
Riconbriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
Aritle: V(lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lamk
Aritle: V(lambda) and J(lambda) -C(lambda) PMID:1904362
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1g lambda chain V region - human
C;Specise: Homo sapiens (man)
C;Specise: Loudous sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S21066
C;Accession: S21066
C;Accession: A; Lecroisey, A; Henschen, A; Ruttyn, Y; Rouger, P; Keil, B.
Protein Seq. Data Anal. 4, 119-324, 1991
A;Title: Partial amino acid sequence of the light chain of human anti-Rh(D) monoclonal
A;Reference number: S21066; MUID:92253545; PMID:1812484
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                     6 LLLTLLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGASSNIGTNDVYWYQQLTGTAPK
                                                                                                                                                                                                                                                                     LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT
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80.8%; Score 995; DB 2;
Best Local Similarity 84.3%; Pred. No. 9.9e-58;
Matches 194; Conservative 13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: S25742
A,Scaus: prellminary; translation not shown
A,Molecule type: mRNA
A,Residues: 1-232 <COM>
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PMID:1904362
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens
Cispecies: Homo sapiens
Cispecies: Homo sapiens
Ricombriato, G.; Klobeck, H.G.
R
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    ŸLIYNNNERPSGVPDRFSGSKSGTSASLAISGLQSDDEADYYCAAWDDSLNGRLLGGGTK 124
                                                                                                                                    61 PARFSGSKSGTSASLAISGLQAEDEADYYCQSYDSSLTAWVFGGGTKLTVLRQPKAAPSV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TLPPFSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                     127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;132-200/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                              185 TPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                               187 TPSKQSNNKYAASSYLSLTPEOWKSHRSYSCQVTHEGSTVEKTVAPTECS
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83.5%; Pred. No. 4.1e-58;
iive 18; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
81.5%; Score 1003.5; DB 2
Best Local Similarity 89.4%; Pred. No. 2.6e-58;
Matches 194; Conservative 9; Mismatches 13;
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Matches 192; Conservative
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gene segments of the human immunoglobulin lamt
PMID:1904362
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QSVLIQPPSASGIPGQRVTISCSGSSSNIGSNVVTWYQQLPGTAPKLLIYINNQRPSGVP 60
                                                        A;Residues: 1-216 <KLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin; pyroglutamic acid
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LLILILIHCAGSWAQSVLIQPPSASGTPGQRVIISCSGSSSNIGGNIVNWYQQLPGRAPK
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                                                                                                                                                                                                                                                                                                                                                                       21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSVT
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                        14; Indels
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81.0%; Pred. No. 6e-56;
                                                                                                                                                                                                                                             80.0%; Score 986; DB 2;
86.1%; Pred. No. 3.5e-57;
ive 16; Mismatches 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S25754
R; Combriato, G; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A; Title: V(lambda) and J(lambda)-C(lambda) gene
A; Reference number: S16439; MUID:91257162; PMID
A; Accession: S25754
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-235 < COM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 YLSLTPEOWKSHKSYSCOVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.0%
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                  Conservative
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Ig lambda chain (Kol) - human
C;Species: Homo sapiens (man)
                             A;Molecule type: protein A;Residues: 1-216 <KLA>
                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 186; Conserv
A; Accession: A42193
                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C)Accession: 82574
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Title: Vulambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: 816439; MUID:91257162; PMID:1904362
A;Accession: 825744
A;Status: preliminary; translation not shown
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C;Species: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                            199
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                                                                                               Gaps
                                                                                                                                                       21 BSVLTQPPSVSGAPGQKVTISCTGSTSNIGG-YDLHWYQQLPGTAPKLLIYDINKRPSGI 79
                                                                                                                                                                                                                      1 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGARYDVNWYQQLPGTAPKLLIYGNTIRPSGV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X57809; NID:g33714; PIDN:CAA40946.1; PID:g33715 C;Superfamily: immunoglobulin Vegion; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin Filds-216/Pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS
                                                                                                                                                                                                                                                                                                                                                                                                                 140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS
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                                                                                               5.
                             Length 213;
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                                                                                               Indels
                                Query Match 80.3%; Score 989.5; DB 2; Best Local Similarity 88.5%; Pred. No. 2.1e-57; Matches 192; Conservative 10; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

80.1%; Score 987; DB 2;
Best Local Similarity 83.0%; Pred. No. 3.3e-57;
Matches 191; Conservative 16; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 SYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig lambda chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-233 <COM>
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19 lambda chain (New) - human (fragment)
19 lambda chain (New) - human (fragment)
19 lambda chain (New) - human (fragment)
19 lambda chain (New) - human)
19 lambda chain (New) - human immunoglobulin fragment Fab New refined at 2.0 A rescalt Fabrace number: A49444; MUID:93066153; PMID:1438175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: sequence modified after extraction from NCBI backbone
A;Note: this sequence report includes corrections based on crystal structure refinement
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;123-191/Domain: immunoglobulin homology <IMM>
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                              64 APKLMIYEVTKRPSGVPNRFSGSKSGNTASLTVSGLQAEDEADYYCSSYAGS-NSLIFGG 122
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                                                                                                                            123 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAAPSV
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                                                                                          124 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS
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                                                                                                                                                                                                                                                        183 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 235
                                                                                                                                                                                                                      184 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 208;
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85.7%; Pred. No. 2.4e-54;
tive 12; Mismatches 9;
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Matches 186; Conservative
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A;Molecule type: protein
A;Residues: 1-208 <SAU>
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C;Date: 07.Jun-1990 #sequence_revision 07-Jun-1990 #text_cnange 41-van-2000
C;Accession: $03401
R;Kratzin, H.D.; Palm, W.; Stangel, M.; Schwidt, W.E.; Friedrich, J.; Hilschmann, N. Biol. Chem. Hoppe-Seyler 370, 263-272, 1989
A;Title: The primary structure of the crystallizable monoclonal immunoglobulin IgG1 Kol. A;Reference number: $03401; MUID:89228564; PMID:2713105
A;Accession: $03401
A;Molecule type: protein
A;Residues: 1-216 -KRAA
A;Note: article in German with English abstract
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetremer; immunoglobulin; pyroglutamic acid
F;131-199/Domain: immunoglobulin homology < IMMA
F;11/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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S14675
Ig lambda chain - human
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C; Accession: S14675; S12445
R; Vasicek, T.J.
Submitted to the EMBL Data Library, February 1990
R; Vasicek, T.J.
Submitted to the EMBL Data Library, February 1990
R; Vasicek, T.J.
Submitted to the EMBL Data Library, February 1990
R; Molecule type: DNA
R; Residues: 1-235 < VASIS
R; Vasicek, T.J.; Leder, P.
J; Exp. Med. 172, 609-620, 1990
A; Title: Structure and expression of the human immunoglobulin lambda genes.
R; Vasicession: S12445
R; Vasice DNA
R; Residues: 1-129 < VASIS
R; Residues: 1-120 < VASIS
R; Re
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76.8%; Score 946; DB 2;
Best Local Similarity 83.3%; Pred. No. 1.4e-54;
Matches 180; Conservative 15; Mismatches 21;
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SEQUENCE (DOT).
MEDLINE=92255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
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Biochemistry 13:1295-1302(1974).
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sapien
                                                                                                                                                                  March 29, 2003, 09:06:23 ; Search time 5.62693 Seconds (without alignments) 1739.566 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                             1 MRVPAQLLGLLLLWLPGARC...........CQVTHEGSTVEKTVAPTECS 236
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P06316 H
P01701 H
P04208 H
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P01846 H
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P01848 H
P01703 H
P01704 H
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P01710
P01713
P20764
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112892 segs, 41476328 residues
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Maximum Match 100%
Listing first 45 summaries
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LAC_FIG
LU11_HUMAN
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34 341 27.7 111 1 LV 36 340.5 27.6 129 1.87 36 37.5 108 11.87 37.5 108 11.87 37.5 108 11.87 37.5 108 11.87 37.5 108 11.87 37.5 108 11.87 37.5 108 11.87 37.5 108 11.87 37.5 26.7 117 11.87 32.6 26.7 117 11.87 32.6 26.5 103 11.87 32.6 26.1 108 11.87 31.8 22.6 10.6 11.87 31.8 22.6 11.7 11.87 31.8 22.6 11.7 11.87 31.8 22.6 11.8 11.8 22.9 106 11.8 21.011.1986 (Rel. 01, Created) 21.011.1986 (Rel. 01, Created) 21.011.1986 (Rel. 01, Last sec. 12.011.1986 (Rel. 01, Last sec. 12.011.1	D HUMA A HUMA A HUMA B HUMA C HUMA C HUMA C HUMA B HUMA A HUMA C HUMA	AL I GNIM	RT;	cation	raniat			~ ~ 0	-64) S.,	ture fa	2 Z	Primar mbda t mino a	N NEWN	bda)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE 294:536-540(1981).

-!- MISCELLANBOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE FERN HARKER, THE NEW PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN HAS THE KERN+ MAKER, AND THE MCG+ MARKER.

-!- MISCELLANBOUS: SIX TANDEM LAMBDA-LYPE GENES WERE IDENTIFIED & THE MISCELLANBOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE MCG SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
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MEDLINE=28206680; PubMed=6273747;
Hieter P.A., HOllis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90133913; PubMed=2515285;
Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
Three-dimensional structure of a light chain dimer crystallized in
water. Conformational flexibility of a molecule in two crystal
forms.";
                                                                                                              MEDLINE-75046825; PubMed=4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
                                                                                                                                                         Saul F.; "The three-dimensional structure of the fab' fragment of a human
"Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995).
                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY .(2.3 ANGSTROMS) OF MCG.
Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
Panadiotopoulos N.;
Morational allomerism and divergent evolution of domains in
immunoglobulin light chains.";
Biochemistry 14:3953-3961(1975).
                                                                                                                                                                                                 myeloma immunoglobulin at 2.0-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
                                                                                                                                                                                                                                                                                                           Fett J.W., Deutsch H.F., "Primary structure of the Mcg lambda chain."; Biochemistry 13:4102-4114(1974).
                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
MEDLINE=75013804; PubMed=4415202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00253; AAA59107.1; -.
EMBL; L38562; AAB6581.1; ALT INIT.
EMBL; X51754; CAB38569.1; ALT_INIT.
EMBL; X51755; CAA36049.1; -.
EMBL; X51755; CAA36051.1; -.
EMBL; X61755; AAM1.92.
EMBL; AMC1585; IGLC1.
Genew; HGNC:5855; IGLC1.
Genew; HGNC:5856; IGLC1.
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InterPro, IPR03597; Ig_cl.
Pfam, PF00047; Ig. 1.
SMART; SM00407; IG_Cl. 1.
PROSITE; PS00290; IG_MHC; 1.
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132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5) (CD179D antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
Length 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                    /FTId=VAR 003900.
T -> K (IN MCG+ MARKER).
FTId=VAR 003901.
R -> K (IN OC2+ MARKER).
/FTId=VAR 003902.
                                                         A -> N (IN MCG+ MARKER).

/FTIG=UAR 003898.
S -> T (IN MCG+ MARKER).
/FTIG=VAR 003899.
S -> G (IN KERN+ MARKER).
                                                                                                                                                                                                                                                                                                                                                                                                     11236 MW; DCD9C7C201C13CC2 CRC64;
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100.0%; Pred. No. 5.3e-37;
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region BL2 precursor.

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Ig lambda cuca...
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMUNOGLOBULIN LAMBDA-LIKE POLYPEPTIDE 1.
J REGION (BY SIMILARITY TO LAMBDA
LIGHT-CHAIN).
C REGION (BY SIMILARITY TO LAMBDA
LIGHT-CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 AQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 THVFGSGTQLTVLSQPKATPSVTLFPPSSEELQANKATLVCLMNDFYPGILTVTWKADGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.8%; Score 527; DB 1; Length 213; Best Local Similarity 52.3%; Pred. No. 5.8e-35; Matches 125; Conservative 15; Mismatches 47; Indels 52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 PITQGVEMTTPSKQSNNKYAASSYLSLTPEQWRSRRSYSCQVMHEGSTVEKTVAPAECS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 RWPLLLIGLAVVTHGLLRPTAASQSRALGP----GAPGGS---SRSSLRSRWGRFLL--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 PVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RVPAQLLGLLL ---- LWLPGARCESVLTOPPSVSGAPGQKVTISCTGSTSNIGGYDLHWY 57
                                                                                            J. Exp. Med. 173:305-311(1991).
--- SUBINIT: Associates non-covalently with VPREBI.
--- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL
--- ELELL LINE (WHICH IS SUFFACE IG NEGATIVE).
--- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
--- DATABASE: NAME-PROW; NOTE-PROW 1:64-67(2000);
           MEDLINE=91108327; PubMed=1703205;
Evans R.J., Hollis G.F.;
"Genomic structure of the human Ig lambda 1 gene suggests that it m
be expressed as an Ig lambda 14.1-like protein or as a canonical B
cell Ig lambda light chain: implications for Ig lambda gene
                                                                                                                                                                                WWW="http://www.ncbi.nlm.nih.gov/prow/guide/696419174_g.htm".
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    Signal.
    POTENTIAL.

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SMART; SM00407; 1Gc1; 1.
PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domain; B-cell;
SIGNAL
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InterPro; IPR003597; Ig_cl.
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MIM; 146770; -
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TISSUE=Lymphoid;
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97
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01-JAN-1988
15-JUL-1999
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LV1G HUMAN
ID LV1G H
AC P06316,
DT 01-JAN-
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Created)
Last sequence update)
Last annotation update)

(Rel. 06, (Rel. 06, 1) (Rel. 38, 1)

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 LLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LLILLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNDYVSWYQQVPGTAPK 65
                                                                                                    SEQUENCE FROM N.A.
MEDLINE-85062823; PubMed-6095199;
Tsujimoto Y., Croce C.M.;
"Molecular cloning of a human immunoglobulin lambda chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subsubgroup.",
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Mammalia; Butheria; Primates; Catarthini; Hominidae; Homo.
NCBI_TaxID=9606;
Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=83186114; PubMed=6404900;
Kamecani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Kamecani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 130;
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72.8%; Pred. No. 3.7e-30;
tive 15; Mismatches 19,
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g lambda chain V-I region NIG-64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X01147, CAA25598.1; -. PIR, A01966, LIHUBL. HSSP, P01703, 7FAB. InterPro; IPR003006; Ig MHC. InterPro; IPR003596; Ig_v.
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Best Local Similarity
                                                     NCBI_TaxID=9606;
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LV2K HUMAN
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Langer B., Steinmetz-Kayne M., Hilschmann N.;
Langer B., Steinmetz-Kayne M., Hilschmann N.;
"The complete amino acid sequence of Bence Jones protein New (lambda-type). Subgroups in the variable part of immunoglobulin L-chains of the lambda-type.";
Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
-!- MISCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.
HSSP; P01703; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSVGMFGGGTRVTVLG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 111;
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111 AA; 11454 MW; A21C6121C18A61E0 CRC64;
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; Pred. No. 1.6e-29;
12; Mismatches 12;
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; l.
SMART; SM00406; IGV, l.
Immunoglobulin V region; Bence-Jones protein.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update
19 lambda chain V-I region NEW.
                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
J. Biochem. 93:421-429(1983).
PIR; A01965; LIHUNG.
HSSP, P01703; 7FRB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 36.9%;
1 Similarity 78.4%;
87; Conservative 13
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
MOD RES 22 89
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Best Local Similarity
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P01701;
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RESULT 6

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MEDLINE=83221661; PubMed=6407018;
Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
Tomplete covalent structure of a human immunoglobulin D: sequence of the lambda light chain.";
Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
PRIS, A01967; LiHUWA.
INTERPRO; IPRO0306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfan, PF00047; ig; 1.
Pfan, PF00047; ig; 1.
Immunoglobulin V region.
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FEBS Lett. 185.139-141(1985).
-!- MISCELLANBOOUST THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN INDIVIDUAL WITH MYELOWA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
PIR; A01971; L2HUNG.
INTERPRO; IPRO03006; Ig MHC.
InterPro; IPRO03596; Ig V.
PHEM: PF00047; ig; 1.
PRART; SM00406; IGV.
Immunoglobulin. Amyloid; Bence-Jones protein.
DISULFID 22 90 BY SIMILARITY.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                     Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
"Amino acid sequence of an amyloidogenic Bence Jones protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVL 130
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109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;
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20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g lambda chain V-II region NIG-84.
                                                                                      20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g lambda chain V-I region WAH.
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J SEGMENT.
BY SIMILARITY.
PRT;
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=9606;
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MEDLINE=85257662; PubMed=2410269; Mihaesco C.; Mihaesco C.; Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.; Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.; Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.; Mihaesco C.; Mihaesco E., Roy J.P., Congrand and antigenic features."; MISCELLANEOUS: RESIDUES 33.36 AND SOME OF THE SEQUENCED PEPTIDES WERE POSITIONED BY HOWOLOGY.

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82220143; PubMed=6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Somatic variants of murine immunoglobulin lambda light chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A. (MOPC 315).
MEDLINE=81148806, PubMed=6259534;
Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
Gefter M.L., Baltimore D.,
"Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 413.5; DB 1; Length 112; 69.4%; Pred. No. 2.5e-26; ative 19; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PDRFSASRSGTSASLAISGLQSEDEADYYCAAWDDSLDGYVFGTGTKVTVL 111
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Monoclonal antibody.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 112
112 Aa; 11789 MW; 748124F079CFFBB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-83014953; PubMed=6812053; Selsing E., Miller J., Wilson R., Storb U.; "Evolution of mouse immunoglobulin lambda genes."; Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 lambda-1 chain C region.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AA
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MEDLINE=71107854; Pubmed=5276767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                        PIR; A25479; LIHUMM.
HSSP; P01703; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 298:380-382(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                    MARKERS.
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P01843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                   21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGTAPKLLIYDINKRPSGI 79
                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novotny J., Franek F., Margolies M.N., Haber B.,
"Amino acid sequence of normal (microheterogeneous) porcine
immunoglobulin lambda chains.",
Biochemistry 16.3776-3772(1977).
-!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MIXTURE OF NORMAL
IMMUNOGLOBULINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).

Sus scrofa (Pig).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 36, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation update)
19-JUL-1999 (Rel. 38, Last annotation update)
19-JUL-1998 (Rel. 38, Last annotation u
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H
                                                                        Query Match 34.5%; Score 424.5; DB 1; Length 112; Best Local Similarity 70.5%; Pred. No. 3.4e-27; Matches 79; Conservative 16; Mismatches 16; Indels 1;
                                                                                                                                                                                                                                                                                          SDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLG 131
                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                      16; Indels
112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 AA; 11003 MW; 3817AAEBD747C396 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 415; DB 1; 74.3%; Pred. No. 1.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig. 1.
SMART; SM00407; ig. 1.
PROSITE; PS00290; IG MHC; 1.
Inmunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 lambda chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AA
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HSSP; P01842; ZMCG.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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P06887;
NON TER , SEQUENCE
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LV1H HUMAN
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NCBI_TaxiD=9606;
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Matches 78;
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LV11 HUMAN
ID LV11 HUMAN
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P01847;
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Matches
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                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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      Appella E.;
"Amino acid sequences of two mouse immunoglobulin lambda chains.";
"Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:590-554 (1971).
Proc. Natl. Acad. Sci. U.S.A. 68:590-554 (1971).
Proc. Chain & I.S.A. CELL LINE PRODUCES 2 LIGHT CHAINS, 1
I-LAMBDA-2 CHAIN & I. ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING
A LANGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
APPEARS COMPLETELY NORMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 OPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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ET -> TE (IN REF. 4).
Q -> E (IN REF. 4).
MISSING (IN REF. 4).
HS -> SH (IN REF. 4).
S -> SG (IN REF. 4).
E -> Q (IN REF. 4).
E -> Q (IN REF. 4).
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EMBL; J00587; AAB59672.1; --
FIR; AQ126; LIMS.
FIR; AQ126; LIMS.
FIR; AQ1084; FRB:
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
FRMAR; SM00407; Ig; 1.
SMART; SM00407; Igc.1; 1.
SMART; SM00407; Igc.1; 1.
SMART; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
NON TER
DISULFID 27 86
INTERCHAIN (WITH HEAV CONFLICT 19 20 ET -> TE (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinoda T., Titani K., Putnam P.W.;
"Amino acid sequence of human lambda chains. II.
peptides and sequence of protein Ha.";
J. Ball. Chem. 245:4475-4487(1970).
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR, PO1703; PO1704.
InterPro, IPR003006; Ig_MHC.
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104
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11575 MV;
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Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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P01700;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                               21 ESVLTOPPSVSGAPGOKVTISCTGSTSN-IGGYDLHWYQQLPGTAPKLLIYDINKRPSGI 79
                                                                                                                                                                                                                                                                                                                                                                            type lambda).";
Baiol. Chem. Hoppe-Sayler 366:617-625(1985).
-!- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED PRECELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED PRECELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED PRECELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED PRECELLANEOUS BY HOMOLOGY.

HISCAPPED 11 THORD BY HOMOLOGY.

InterPro; IPRO03006; Ig MHC.

InterPro; IPRO03596; Ig V.

Pfam; PF00047; ig; 1.

SMART; SMO046; IGY. 1.

Immunoglobulin V region; Amyloid; Glycoprotein.

CARBOHYD 104 N.LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=66000126; PubMed=3929803;
Toft K.G., Sletten K., Husby G.;
"The amino-acid sequence of the variable region of a carbohydrate-containing amyloid fibril protein EPS (immunoglobulin light chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 402; DB 1; Length 109; 70.3%; Pred. No. 2e-25; tive 16; Mismatches 15; Indels
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
MD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
NON_TER 112 112
SEQUENCE 112 AA; 11896 MW.
                                                                                                                                                                                                                                            33.1%; Score 407.5; DB 1; Length ilarity 71.2%; Pred. No. 7.6e-26; Conservative 17; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 AA; 11414 MW; 556A313E24D5AC73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-07N-1998 (Rel. 06, Created)
01-07N-1998 (Rel. 06, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1G lambda chain V-I region EPS.
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                                                                                                                                                                                                                                                                       Local Similarity
hes 79; Conserv
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RESULT 15
LV2B_HUMAN
ID _LV2B_HUMAN
                 MOD RES
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"Pattern of antibody structure. The amino acid sequence of a monoclonal immunoglobulin L-chain of lambde-type, subgroup I (Bence-Jones-protein Vor.). A contribution to the elucidation of the origin of antibody specificity.", Hoppe-Seyler's Z. Physiol. Chem. 356:1413-1444(1975).

"In MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER."

"IN MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. 197:177-183(1981).
-!- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 104 INTERCHAIN (WITH HEAVY CHAIN) 105 AA; 11484 MW; B427513272E8663D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFICITY.

PIR; A02130; L7RB.
HSSP; POING 1278.

INTERPC: 1PR003306; Ig MHC.
INTERPC: 1PR003597; Ig_c1.
PEam; PF00047; Ig; 1.
PROSITE; PS00290; IG MHC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin C region.
NOW TER

DISULFID

DISULFID

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SEQUENCE

105 AA; 11484 MW; B427513272E8663D CR
                                                                                                                                                                                                                                                                                                                                                                       Garcia I., Jaton J.-C., "The primary structure of the constant region of immunoglobulin lambda-chains.";
21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Bence-Jones protein.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-I region VOR.
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HSSP; P01703; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 76; Conservative
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P01699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                  61 SNRFSGSKSGKTASLTISGLQVEDEADYYCCSYAGN-STRVFGGGTRVTVL 110
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-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

PIR, A019-0; L2HUNI.

HSSP; PO1709; 2MCG.

InterPro; IPR003506; Ig_MC.

InterPro; IPR003506; Ig_v.

Pfam; PP00047; ig; I.

Immunoglobulin V region; Bence-Jones protein; Glycoprotein.

MOD_RES.

InterPro; IRV region; Bence-Jones Protein; Glycoprotein.
                                                                                                                           Query Match 32.1%; Score 396; DB 1; Length 111; Best Local Similarity 65.8%; Pred. No. 6.1e-25; Matches 73; Conservative 20; Mismatches 18; Indels
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PYRROLIDONE CARBOXYLIC ACID
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N-LINKED (GLCNAC. . .).
  1 1 PYRROLIDONE CARBOXY 22 89 BY SIMILARITY. 111 111 AA; 11514 MW; 21D9F64250DFC8E0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human)
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TISSUE=TONSIL;
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Q8WUK4
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Q84684 mus musculu
Q846260 homo sapien
Q91402 mus musculu
Q8VCi6 mus musculu
Q8VCi6 mus musculu
Q99m37 mus musculu
Q99m37 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96169 homo sapien
Q8wuk3 homo sapien
Q99m11 mus musculu
Q8tcj5 homo sapien
                                                       March 29, 2003, 09:06:23 ; Search time 21.4044 Seconds (without alignments) 2271.829 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8wuk4 homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                 1 MRVPAQLLGLLLLMLPGARC.....CQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8wtu6
Q96e61
Q8tbc9
                                                                                                                                                                                          671580
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                  671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8WUK4
Q8WTU6
Q9EE61
Q8TBC9
Q9E169
Q8WUK3
Q9W11
Q8TCJ5
Q8VCP0
Q9D8W4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TCD0
Q91W12
Q8R062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VC16
Q99M37
Q91WS9
                                                                                                                                                                                                                                                                                                                                                                                       sp_rodent:*
sp_virus:*
sp_virus:*
sp_vortebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                 sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                       sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                              US-09-758-173-10
                                                                                                                                                                                                                                                                                                                                                                            sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                               SPTREMBL 21:*
                                                                                                                                                                                                                                                                                                                     sp_human: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                          88:
100:
111:
112:
114:
115:
                                                                                                         Perfect score:
                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1045
1045
991.5
988
805.5
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472
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461.5
453.5
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                                                                                                                   Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
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	Q87029 mus musculu Q87028 mus musculu Q87135 mus musculu	homod		homod	096jdl homo sapien	٠.	Q90544 ginglymosto	Q9ul82 homo sapien	Q90524 ginglymosto			0	O9ul78 homo sapien		6 gina	~	Q90530 ginglymosto	_		۶	Ogn410 achiatosoma			enm o
Q91WF8 Q8TE63 ORVC55	Q8R028 Q9R1A5	Q96SB0	096JD0 099JC1	Q96JD2	Q96JD1	90SN6Ö	090544	Q9UL82	090524	092589	090529	Q8VDD0	Q9UL78	Q8TC77	090536	Q9JL78	05060	Q8R3V9	090568	OSUL86	09U410	Q96SA9	Q9UL85	Q8VEA0
11 4 1	111	4.	4 7	4	4	4	13	4	13	디	13	11	4	4	13	11	13	11	13	4	ß	4	4	11
234 110	234	108	105 105	112	112	107	684	107	268	127	267	134	109	471	257	101	259	469	252	109	106	107	109	484
35.6	33.2	31.2	30.5	30.3	28.4	26.9	m	23.3	23.0	22.9	21.8	21.6	21.3	ä	20.9	20.7	20.3	20.3	20.3	20.0	19.9	19.9	19.7	19.6
447.5	433.5	385	375.5	373	349.5	332	292.5	287.5	283	282.5	268.5	265.5	262	260	258	255	250.5	250.5	249.5	246	245	245	243	241.5
118	20	22	24	25	26	27	80 6	62.	30	31	35	33	34	32	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

| December 2012 (TrEMBLrel. 20, Created) | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-00 | 10-000 | 10-000 | 10-000 | 10-000 | 10-000 | 10-000 | 10-000 | 10-000 | 10-000 | 10-000 | 10-000 |

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotheital 24.9 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                            TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8TBC9
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          OC REPRESENTATION OC DR REPRESENTATION OC DR REPRESENTATION OC DR REPRESENTATION OCCUPATION OCCUPAT
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TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
                                                                                                                                            126 TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 KLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDYSLSASGVFGGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 TRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LLILLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LIGLILLWIPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                    185 TTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                           TITPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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84.8%; Score 1045; DB 4; Length 237;
Best Local Similarity 88.4%; Pred. No. 6.1e-82;
Matches 205; Conservative 10; Mismatches 15; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 24.9 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96E61, CTEMBLrel. 19, Created)
01-DEC-2001 (TTEMBLrel. 19, Last sequence update)
01-DEC-2001 (TTEMBLrel. 19, Last sequence update)
UNAR-2002 (TTEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:17259).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 AA
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QUANTUG

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OR TO 1-M

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Q96E61
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125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.1%; Score 888; DB 4; Length 233; Best Local Similarity 74.0%; Pred. No. 1.8e-68; Matches 174; Conservative 16; Mismatches 33; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVF 121
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                  7 LIGILLILWIPGARCESVITQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 LLWLP------GARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLP 61
                                                                                                                                                                                                                                                                                                                                                                                                        6 LLLTLLAHCTGSWAQSVLAQPPSVSGAPGQTVTISCTGSSTNIGAGYAVHWYQQFPGAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAWIPLLIPLITICTGSEASYELTQPPSVSVSPGQTARITCSGDA--LPKQYAYWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                            Soore 991.5; DB 4; Length Similarity 83.1%; Pred. No. 2.4e-77; 92; Conservative 12; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 TKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
Straubberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1; -.
InterPro; 19700306; 1g_MHC.
Pfam; PF00047; 19; 2.
PROSITE; PS00290; 1G_MHC; UNKNOWN 1.
SEQUENCE 236 AA; 24712 WW; 7EC9FB3622FED957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=PRIMARY B-CELLS;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022823; AAH22823.1; -.
Hypothetical protein.
SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
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136 APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PTNMIYGDDLRPSGVSDRFSGSIDSSSNSAFLTIQNVQADDEADYYCQSYSSGI--RVFG 121
                                                                                                                                                                                                                                                                                                                                                                 79 ISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ---VFGGGTRLTVLGQPKA 135
                                                                                                                                                                                                                                       9; Gapa
                                                                                                                                                                                                                                                                                                         22 VLTQPPSASAFLGASIKLTCTLSREH-SSYTIEWYQQRPGRSPQYIMKVKSDGSHNKGDG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 PKLLIYDINKRPSGISDRFSGS--KSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFG 122
                                                                                                                                                                                                                                                                                23 VLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIY----DINKRPSG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 APLLLVFLHHITGSCAQLVLTQPSSVSTSLGSTAKLPCKASTGNIGDSYVNWYQQYMGRS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AQLLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                          62.3%; Score 767.5; DB 4; Length 240; 69.2%; Pred. No. 4.2e-58; trive 21; Mismatches 38; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.6%; Score 722; DB 11; Length 235; Best Local Similarity 61.1%; Pred. No. 3.3e-54; Matches 143; Conservative 29; Mismatches 58; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002129; AAH02129.1; -.
                  ### PF00047; 19; 2.

SMART; SM00409; IG; 2.

SMART; SM00409; IG; 2.

SWART; SM00406; IGc1, 1.

PROSITE; PS00290; IG MHC; UNKNOWN_1.

Hypothetical protein.

SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 25.4 kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Dram; PF00047; 19; 2. | SMART; SM00409; 1G; 2. | SMART; SM00409; 1G; 2. | SMART; SM00407; 1GC1; 1. | SMART; SM00410; 1G_1; 1. | SMART; SM00410; 1G_1ike; 2. | PROSITE; PS00290; 1G_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; IG.
InterPro; IPR003597; IG.
InterPro; IPR003609; IG.Ike.
InterPro; IPR003506; IG.
InterPro; IPR003596; IG.V.
      InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                     Matches 153; Conservative
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                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Q99M11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:12849).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
179 GVÉTTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.4%; Score 805.5; DB 4; Length 233; Best Local Similarity 70.0%; Pred. No. 2.2e-61; Matches 161; Conservative 21; Mismatches 45; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007782, AA407792.1;
InterPro; IPR003598; Ig c2.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PP0047; ig; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS00178; AA_TRNA_LIGASE I; UNKNOWN_I.
PROSITE; PS00178; AA_TRNA_LIGASE I; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straudberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020236; AAH20236.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogiobulin domain. -
SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBWUK3;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.0 kba protein.
Homo sapiens (Human).
                                                                                                            233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 240 AA
                                                                                                         PRT;
                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          TISSUE=B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=TONSIL;
                                                                                                     Q96169
Q96169;
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QBWUK3
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Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
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1810027001RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9D8W4;
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                     123 GGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 182
                                               122 GGTKLTVLSOPKTSPSVTLFPPSSEELETNKATLVCTISDFYPGVVTVDWKADGTPVTOG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 GOPKAAPSVILFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITPSK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GQPKAAPSVTLFPPSSEELQANKATLVCLISDPYPGAVTVAWKADSSPVKAGVETTTPSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muxinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                     Query Match

44.7%; Score 551; DB 4; Length 106;
Best Local Similarity 99.1%; Pred. No. 5.4e-40;
Matches 105; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.,
Strausberg R.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
REBL; BC019474; AAAH)9474.1;
A InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003569; Ig.
R InterPro; IPR003056; Ig.
R Pfam; PF00047; ig; 2.
R SWART; SW00406; IG; 2.
R SWART; SW00406; IGC; 1.
R PROSITE; PS00250; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UDN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 Kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA.
                                                                                                                                                                                                                                                               106 AA
                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotatio
Hypothetical 11.3 kDa protein (Fragment)
DKF2P667J0810.
                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ruchl P., Lewis S., Matsuo T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Bolt C., Fletcher C., Fulita M., Garibldi M.,
Brownstein M.J., Bult C., Fletcher C., Fulita M., Garibldi M.,
Lyons P., Marchionni L., Mashima J., Mazarelli J., Mondbarts P.,
Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Stoch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Wilming L.,
Havsehizaki A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                    117 TFGSGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 175
                                                                                                                                                                                                                                                                                                        60 LPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 VFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV 179
                                                                                Gaps
                                                                                                                                                        1 MRVPAQLLGLLLWLPGARCESVLTQ-PPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQ 59
                                                                                                                                                                                                    180 KAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                6
    DB 11; Length 234;
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Query Match
39.7%; Score 488.5; DB 11; Length
Best Local Similarity 44.8%; Pred. No. 3.6e-34;
Matches 107; Conservative 42; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00407; IGC1; 1.
SMSRT; S800209; IG MHC; UNKNOWN 1.
SEQUENCE 130 AA; I4253 MW; 438197975E766E54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1916426; 1810027001Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK007622; BAB25142.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
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77 SGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTRLTVLGQPKAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                    137 PSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV-ETTTPSKQSNNK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 VFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 LPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 KPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYYCQQY--SQFPF 116
                                                                                                                                                                                                                                                                                                                                                   18 ARCESVLTQPPSV-SGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRVPAQLLGLLLLWLPGARCESVLTQ-PPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MMSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCSAS-QGISNY-LNWYQQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 KAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                              37.8%; Score 466; DB 11; Length 235; 44.1%; Pred. No. 3.1e-32; tive 47; Mismatches 67; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databages. EMBL, EC027418; AAH27418.1; -. Hypothetical protein. SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
                                                                                 Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                    EMBL; BC006643; AAH06643.1; -.
InterPro; IPR03006; Ig_MHC.
Pfam, PF00047; ig; 2.
PROSTIE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 235 AA; Ž6021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 YAASSYLSLIPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 YSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBR062;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.2e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical 25.9 kba protein.
Mus musculus (Mouse),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.48;
                                                                                                                                                                                                                                                                                        98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                   [1]
SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                              Query Match
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                        SARARAS
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                                                                                                                                                               66 WKVDGTPVTQGMETTQPSKQSNNKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKSLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 SPVKAG--VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 YQQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 NAQVEGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 YDSSLNAQVFGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA 171
                   0; Gaps
                                                                            6 HESISQCWVFGGGTKLTVLGQPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.3%; Score 472; DB 4; Length 239;
Best Local Similarity 42.0%; Pred. No. 9.7e-33;
Matches 102; Conservative 52; Mismatches 77; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRVPAQLLGLLLLWLPGARCESVLTQPP-SVSGAPGQKVTISCTGSTSNI---GGYDLHW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                   23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAH22362.1; -.
Hypothetical protein.
SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03B71D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26, 2 kpa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                     239 AA
                 Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown (protein for MGC:6582).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                      232 PTECS 236
                                                                                                                                                                                                                                                           126 RADCS 130
87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 GEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91W12;
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             Matches
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HSSP; P01679; 2FBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YOOLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS--QSTH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 NAQVEGGTRITVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 SPVKAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kDa protein.
Hypothetical 26.3 kDa protein.
Buka musculus (Mouse).
Manamalia Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                         Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.5%; Score 461.5; DB 11; Length 238; 40.9%; Pred. No. 7.7e-32; Live 53; Mismatches 79; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                     Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019760; AAH19760.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR00306; Ig.MHC.
InterPro; IPR00306; Ig.V.
Pfam; PR00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG.; 1.
PROSITE; PS00290; IG.MHC; UNKNOWN_1.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002(035; AAH02035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created).
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.2 kba protein.
Mus musculus (Mouse).
                                                                             238 AA
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                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.9%
Matches 99; Conservative
                                                                          PRELIMINARY;
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Interpro; IPR003599; Ig.
Interpro; IPR003599; Ig.
Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003066; Ig_WC.
Interpro; IPR00306; Ig_WC.
Interpro; IPR00306; Ig_WC.
Interpro; IPR00306; Ig_WC.
Interpro; IPR00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00410; IG_like; 1.
INTERPRO; IG_MHC; UNKNOWN_1.
INTERPRO; IG_MHC; UNKNOWN_1.
INTERPRO; INTERPRO; IG_MHC; UNKNOWN_1.
INTERPRO; INTERPRO; IG_MHC; INTERPRO; IG_MHC; UNKNOWN_1.
INTERPRO; INTE
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March 29, 2003, 09:06:23 ; Search time 24.273 Seconds (without alignments) 1295.559 Million cell updates/sec
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                           Run on:
```

US-09-758-173-10 1232 1 MRVPAQLLGLLLLWLPGARC.......CQVTHEGSTVEKTVAPTECS 236 Perfect score: Seguence:

Scoring table:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** 

Total number of hits satisfying chosen parameters: 908470 segs, 133250620 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A Geneseq 101002:\* Database :

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
3: /SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:\*
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110: /SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:\*
111: /SIDS2/gcgdata/geneseqg-embl/AA1982.DAT:\*
112: /SIDS2/gcgdata/geneseqg-embl/AA1992.DAT:\*
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122: /SIDS2/gcgdata/geneseqg/geneseqg-embl/AA1990.DAT:\*
123: /SIDS2/gcgdata/geneseqg/geneseqg-embl/AA1990.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Anti-HIV-1 recombi Primatised anti-hu Macaque primatized Protein sequence o Human immune syste Monoclonal antibod Novel human diagno Macaque primatized Protein sequence o Primatised anti-hu Description SUMMARIES AAU11645 AAW01821 AAB36209 AAW88465 ABG23083 AAR42163 AAW01817 AAW63760 AAU11538 AAW63764 П 119 119 119 119 119 В Query Match Length 1000.0 999.8 885.4 881.7 881.2 799.5 799.0 1232 1232 1229 1052.5 1001 973 973 Result

Antibody HB4CE 142	α		immine avat	human diagn	tvpe	Plasmid scPv (CC046	Antibody D light c	Variable and first	Human type antihum	Human type antihum	human	Novel human diagno	Human type antihum	human	l human		1 human	n prote	human			Human secreted pro		Human secreted pro	Novel human diagno	Becre		novel	EST en	novel	ovaria		D4 mon	Human cancer assoc	
AAW40533	ABG26352				AAG64472	ABB06275		AAB30594	AAG64474	AAG64476	ABG12886	ABG19296	AAG64470	ABG19301	ABG19290	ABG19291	ABG22850	AAM78781	ABG19298	AAB15547	AAU08381	AAW75214	AAP81260	AAW75231	ABG19299	AAU82012	ABG19297	AAU14412	AAM23527	AAU14176	ABP41361	ABG19295	AAW14924	AAB43979	
19	22	22	22	22	22	23	14	21	22	22	22	22	22	22	22	22	22	22	22	21	22	19	σ	13	22	23	22	22	22	22	23	22	18	21	
217	248	235	235	236	235	614	235	219	235	235	249	244	235	250	235	251	236	235	236	235	218	235	233	235	238	233	238	232	232	231	269	247	233	244	
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11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

Monoclonal antibody, Mab, macaque; light chain, primate, antigen; CD80; CD86; inhibitor: immunosuppressant; treatment; autoimmune disease; IL-2; T cell/b cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation. Macaque primatized 16C10 light chain protein. AAW63764 standard; Protein; 236 AA 29-SEP-1998 (first entry) AAW63764 

Macaca fascicularis

WO9819706-A1. 14-MAY-1998.

97WO-US19906 29-OCT-1997;

96US-0746361 (IDEC-) IDEC PHARM CORP 08-NOV-1996;

Hanna N; Anderson DR, Brams P,

WPI; 1998-286601/25. N-PSDB; AAV35488.

us-09-758-173-10.rag

```
This sequence represents a primatized form of the antibody 16C10 light chain from macaque. This sequence is used in a method which studies new monclonal antibodies (Mab's) that bind selectively to 81.1 (CD80) or to 87.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving 7 cell/B cell interactions, particularly autoinmune diseases, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple selerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab on be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunospens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking BJ/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression and class of antigen-specific immunosuppression and antigen-specific immunosuppression and class of the season and class of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective, apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B Cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graff-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1232; DB 19; Length 236; 100.0%; Pred. No. 1.2e-66; cive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU11645 standard; Protein; 236 AA
                                                                                                                                          5a; 87pp; English.
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Matches 236; Conservative
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Chimeric - Macaca sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Macaca sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA;
                                                                                                                                       Example 7; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200189567-A1
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducting the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell lymphoma, B cell lymphoma, B cell lymphoma, and autoimmune diseases such as B call oppathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease, and ulcerative colltis, food-related allergies e.g. migraine, chinitis and eczema, and other types of allergies. The present protein sequence represents the light chain of 16C10, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                  Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGTAPKLLIYDINKKPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRVPAQLLGLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGVETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1232; DB 23; Length 236; Best Local Similarity 100.0%; Pred. No. 1.2e-66; Matches 236; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primatised anti-human B7.1 antigen antibody 16C10 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ.
                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Fig 5a; 89pp; English.
                                                                                                                                                           Anderson DR, Hanna N, Brams P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW01821 standard; Protein; 236
                     22-MAY-2001; 2001WO-US16364.
                                                                22-MAY-2000; 2000US-0576424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                              (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used in the invention interleukin-2 (IL-2).
                                                                                                                                                                                                      WPI; 2002-089895/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA;
                                                                                                                                                                                                                            N-PSDB; AAS17246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW01821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                             allergy
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Baughn MR;

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The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPP). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation disease. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, cronn's adiease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, theumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LLITLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system associated protein; HISAP-7; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LIGILILIMIPGARCESVITQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 RLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 KLLIYGSRNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGVVFGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIPSKOSNNKYAASSYLSLTPEOWKSHRSYSCOVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.4%; Score 1052.5; DB 22; Lengt
88.3%; Pred. No. 6.6e-56;
tive 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody 4B5 light chain variable region.
                                                                                                                                                                                                                                                                                                                                      Corley NC, Guegler KJ,
                                                 infection; autoimmune disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Column 59-62; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
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                                                                                                                                                                                                                98US-0049672
                                                                                                                                                                                                                                                       98US-0049672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                      e H, Lal P,
Au-Young J;
                                                                                                                                                                                                                                                                                             (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-030926/04.
N-PSDB; AAC66525.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA;
                                                                                                                                                                                                                                                                                                                                      Yue H,
                                                                                                                                                                                                              27-MAR-1998;
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                       27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                            Hillman JL,
                                                                                                                              US6135941-A
                                                                                                                                                                       24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human heavy antiable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7Cl0 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
primàtised antibody, B7 antigen, CD28, immunosuppressive, autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1229; DB 18;
Pred. No. 1.8e-66;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   Shestowsky WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated protein HISAP-7.
                                                                                                                                                                                                                                                                                                                                                                                                   Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Fig 10A; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36209 standard; protein; 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.8%;
99.6%;
                                                                                                                                                                                                                                                                        96WO-US10053.
                                                                                                                                                                                                                                                                                                                 95US-0487550
                                                                                                                        Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                        (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                   Brams P,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-108638/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT62512
                                                                                                                                                                                                                                                                                                                                                                                                Anderson DR,
                                                                                                                                                                                                                                                                      06-JUN-1996;
                                                                                                                                                                                      WO9640878-A1
                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2001
                                                                                                                                                                                                                               19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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187 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
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                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide comprises the light chain variable region of the recombinant human monoclonal antibody (MAD) 4B5. 4B5 recognises antibodies. Antibodies apecific for GD2 antibodies. Antibodies specific for GD2 antibodies. Antibodies specific for GD2 recognise various cancers including glioblastoma, meloplastoma, malignant and/or metastatic melanoma, breast cancercinoma, malignant and/or metastatic melanoma, breast cancercinoma, uluq adenocarcinoma, mall cell lung carcinoma, colon adenocarcinoma and prostate adenocarcinoma. The invention antibodies specific for GD2. These derivatives, or antigen binding fragments, comprise regions of the 4B5 VD1 junction and regions spanning the 4B5 CDRs. Other derivatives include Fab, F(ab))2, creft and isolated heavy and light chains (see also AAW88464). Polynucleotide fragments (see AAX6951-54) encoding 4B5 antibody vergions are also provided, and therapeutic plasmids and vectors, including vaccinia virus vectors, comprising these polynucleotides. Control of the shown to mimic GD2, and is particularly useful in generating a host immune response to cancer. Products of the invention can be used in the detection and treatment of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 LIVLGQPKAAPSVTLFPPSSEELQANKPTLVCLISDFYPGAVTVAWKADSSPVKAGVETT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LLITILITHCAGSWAQSVLIQPPSASGTPGQRVIISCSGSNSNIGSKTVNWYQQLPGTAPK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
                                                                                                                                                                                                                                                                                                      New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylactic therapy to reduce risk of recurrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      astrocytoma, oligodendroglioma, ependymoma, medulloblastoma, primitive neural eccodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and large cell lung adenocarcinomas, small and large cell lung adenocarcinomas, epithelial adenocarcinoma, and liver metastases, hepatoma, cholanglocarcinoma, breast tumours such as ductal adenocarcinoma, squamous and adenocarcinoma is denocarcinoma, squamous and adenocarcinoma of the uterine cervix, uterine and ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epithelial carcinoma, prostatic adenocarcinoma, transitional squamous cell carcinoma of the bladder, B and T cell lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia, malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 81.7%; Score 1006; DB 20; Length 235; Best Local Similarity 83.9%; Pred. No. 4e-53; Matches 193; Conservative 14; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 81; 83pp; English
                                                                                                                                                                                         (NOVO-) NOVOPHARM BIOTECH INC
                                                                                                                                                          97US-0051945.
                                                                                                                             98WO-IB01046.
                                                                                                                                                                                                                                                        WPI; 1999-120769/10.
GD2 antigen; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 AA;
                                                                                                                                                                                                                                                                         N-PSDB; AAX06953
                                 Homo sapiens
                                                                                                                                                           38-JUL-1997;
                                                              WO9902545-A2
                                                                                                                            08-JUL-1998;
                                                                                            21-JAN-1999
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                                                                                                                                                                                                                         Jan MD;
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the inventor centers to isolate polymorecule it, and and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymorlectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical in solicy and of sorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human conducts data for this patent did not appear in the printed a diagnostic amino acid sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
186 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.2%; Score 1001; DB 22;
83.5%; Pred. No. 8e-53;
live 18; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 53442; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #23074.
                                                                                                                                                                                                                                      ABG23083 standard; Protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 83.54
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS87270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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7 LLGLLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66

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AAW01817;
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AAW01817
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                                                                                                                                                                                                                  127 LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
                                                                                      7 LLLTLLTLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGASSNIGTNDVYWYQQLTGTAPK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody; Warneutralising monoclonal antibody; immunoglobulin; AIDS; acquired immune defliciency syndrome; chimeric antibody; surface glycoprotein gp120; V3 loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EBV-transformed cell lines and mouse-human heterohybridomas producing human MAbs specific for the gp120 V3 loop of HIV-1 MN isolate were obtained. MAb 47-52D was found to recognise the tetrapeptide motif GPGR, i.e. the Principal Neutralising Determinant common to the V3 loop of different HIV isolates. A recombinant Ab was produced in which the L chain V region was derived from 47-52D and to which a signal sequence and a L chain intronic sequence are appended, fused to a fragment contg. a short intronic segment of the human lambda 2 C region and the human lambda 2 constant encoding domain.
                                                              LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR
                                                                                                                                                                                LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant human antibody - with HIV neutralising activity against at least two isolates, useful for preventing or treating
                                                                                                                                                                                                                                                                                                                                  TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                   TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-HIV-1 recombinant antibody 447-52D light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfarr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson LS, Mark GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR42163 standard; Protein; 217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Fig 2B; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against at least two isolate
infection in diagnosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93WO-US02629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-0861701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emini EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JOHN/) JOHNSON L S. (PFAR/) PFARR D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-336600/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ49835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9319785-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conley AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR42163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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                                                              67
                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
AAR42163
1D AAR42163
1D AAR42163
1D AAR42163
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2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes (see also AAT62509 and AAT62510) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                   180
61 DRFSGSKSGTSATLGITGLQTGDEADYFCATWDSGLSADWVFGGGTKLTVLSQPKAAPSV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
                                                                        121 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS
                                                TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS
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7
                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; soriasis; type I diabetes mellitus; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                      Primatised anti-human B7.1 antigen antibody 7C10 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%; Score 973; DB 18;
80.1%; Pred. No. 3.7e-51;
live 13; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shestowsky WS;
                                                                                                                       SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                         SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                AAW01817 standard; Protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 1 diabetes mellitus, grait
hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 8A; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US10053,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0487550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric Macaca cynomolgus;
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.1%
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brams P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-108638/10.
N-PSDB; AAT62509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640878-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                     25-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-1996.
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Gaps

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Indels

15;

11; Mismatches

Best Local Similarity 87.6\* Matches 190; Conservative

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DB 14; Length 217;

79.5%; Score 979.5; DB 1487.6%; Pred. No. 1.4e-51;

21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80

i.e. it inhibits

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AAU11538;
                                                           Sequence
                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a primatized form of the antibody 7C10 light chair from macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new monclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerois, graft vs. con the diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAb'can be conjugated to a drug or toxin. MAb's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAb's are optionally combined with other proteins or small wolecule immunosuppressants. Blocking B7/CD28 interactions
                                                                                                                                                                                                                                                                                                                                                                                                                   CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; r cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;
                                                                                       59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
                                                                                                                               121 FGGGTRLTVLGOPKAAPSVTLFPPSSEELQANKATLVCLISDFVPGAVTVAWKADSSPVK 180
                                                                                                                                                           FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                       PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
               9
                                          1 MRVPAQLIGLILLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
               MRVPAQLLGLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                                                                                                                                                          236
                                                                                                                                                                                                         AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                           AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                               Macaque primatized 7C10 light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells, e.g. graft rejection or tumours
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                                                                                                                                                                                                                                                                                            AAW63760 standard; Protein; 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US19906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0746361
                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-286601/25.
N-PSDB; AAV35484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9819706-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1997;
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Protein sequence of primatised form of the light chain of 7C10 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                         1 MRVPAQLIGILILMIPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 FGGGTRVTVLGOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                     5
induces long-term, antigen-specific immunosuppression, i.e. : production of interleukin-2 (\rm IL-2), T cell proliferation and antigen-specific immunoglobulin G (\rm IGG) responses.
                                                                                                                                                                                                              Length 234;
                                                                                                                                                                                                                  79.0%; Score 973; DB 19;
80.1%; Pred. No. 3.7e-51;
                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU11538 standard; Protein; 234 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŭ
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                                                                                                                                                                                                                                                     Best Local Similarity 80.10
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Homo sapiens.
Chimeric - Macaca sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson DR, Hanna
                                                                                                                                                  234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS17242
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96JP-0246825

30-AUG-1996;

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cancer where B cells promote the growth and/or metastasis of tumours, B call lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, and autofimmune diseases such as indipopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistence to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present protein sequence represents the light chain of 7010, a primatised antibody used in the inventor to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRVPAQLIGILILWLPGARCESVITQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region (CDR)-2;
sequence claimed in claim 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxypeptidase; bovine pancreas; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.0%; Score 973; DB 23; Length 234; 80.1%; Pred. No. 3.7e-51; ive 13; Mismatches 32; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    porcine pancreas; radioimminoimaging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-2 (IL-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AA;
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Region
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                                                                                                                                                                                             This represents a antibody HB4C5 light chain. This antibody light chain or its fragment is specific for carboxypeptidase from bovine or porcine pancraes and is reactive with human cancer tissue. The antibody light chain and its fragment can be used for preparation of a cancer radioimmunoimaging reagent and therapeutic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                            DRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGGTRLTVLGQPKAAPSV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                         New antibody light chain or its fragment - useful for preparation of therapeutic(s) or cancer radio-immuno-imaging agent(s)
                                                                                                                                                                                                                                                                                                                                                                                      21 ESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPKLLIYDINKRPSGIS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                            DRFSGSKSGTSATLGITGLQTGDEADYYCATWTSILRVNWLFGGGTKLTVLGQPKAAPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS
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                                                                                                                                                                                                                                                                                                            78.9%; Score 971.5; DB 19; Length 217; 86.6%; Pred. No. 4.3e-51; ive 11; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYLSLTPEOWKSHRSYSCOVIHEGSTVEKTVAPTECS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #26343.
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                                                                                                                                                                  Claim 10; Fig 11; 20pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                         Best Local Similarity 86.69
Matches 188; Conservative
                                                      (MOMI ) MORINAGA & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8-FEB-2002 (first entry)
                                                                                WPI; 1998-244364/22
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N-PSDB; AAS90539.
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                                                                                               N-PSDB; AAV11293
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                                                                                                                                                                                                                                                                                                              Query Match
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27-MAR-1998;
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             27-MAR-1998;
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                                                                                     Hillman JL,
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                                                                        Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                          interintal televices to isolate polymericate 1,1 and and polypeptide (II) sequences. (I) be useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The oblymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) to to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical in sorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human once the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 SPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQLPGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PAWPAGALLITILITHCAVPGSWAQSVLTQAPSASGTPGQRVTISCSGSSSNIGNNPVNWY 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PAQLLGLLLLWL-----PGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system associated protein; HISAP-10; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 SPVKAGVETNKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
             New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Indels
                                                                                                                    invention relates to isolated polynucleotide (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%; Score 968.5; DB 2
79.2%; Pred. No. 7.4e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches
                                                                                       Claim 20; SEQ ID No 56711; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; autoimmune disease; cancer.
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Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AA;
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                                                           biodiversity
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AAB36212
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The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPB). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, theumatcoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
                                                                                                                                                                                                                                                                                                                New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYD-LHWYQQLPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 APKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 APKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYVGN-NIVVFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 GTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLJSDFYPGAVTVAWKADSSPVKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ALLFLTLLTQGTGSWAQSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQSPGT
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                                                                                                                        Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.3%; Score 965; DB 22; Length 235;
80.3%; Pred. No. 1.1e-50;
iive 19; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ETTTPSKOSNNKYAASSYLSLTPEOWKSHRSYSCOVTHEGSTVEKTVAPTECS
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                                                                                                                           Guegler KJ,
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                                                                                                                           Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Column 65-68; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ź
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98US-0049672
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Matches 187; Conservative
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                                                            (INCY-) INCYTE PHARM INC
                                                                                                                        ue H, Lal P,
Au-Young J;
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                                                                                                                                                     number of human immune system associated proteins (HISAPS). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
                                                                                                                                                nces for a
These can be
                                                                        New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
                                                                                                                                                                                                                                                                                                                                                                         185
                                                                                                                                                                                                                                                                                                                                                            LLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGTR 126
                                                                                                                                                                                                                                                                                                                                                                                                        LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 186
                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                               LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK 66
                                                                                                                                                                                                                                                                                                                             The present invention provides the coding and protein sequences for number of human immune system associated proteins (HISADS)
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food supplement; medical imaging; diagnostic; genetic disorder
              Baughn MR;
                                                                                                                                                                                                                                                                   78.3%; Score 965; DB 22; Length 235; 80.0%; Pred. No. 1.1e-50; .ive 20; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #19284.
            Corley NC,
                                                                                                                      Claim 1; Column 69-72; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG19293 standard; Protein; 236
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23-AUG-2000; 2000US-0649167.
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Matches 184; Conservative
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           e H, Lal P,
Au-Young J;
                                          2001-030926/04.
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                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                               235 AA;
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                                                    N-PSDB; AAC66530
           Yue H,
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          Tang YT, Yu
Hillman JL,
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, complete the polymerase chair reaction (PECR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The color identifying expressed genes. (I) is useful in gene therapy techniques complete for identifying expressed genes. (I) is useful in gene therapy techniques complete for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as companied of stressing (II). (II) and (II) and (II) and (II) are useful in medical imaging of stressing (II). (I) and (II) are useful in medical consorters involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in classomatics, forensics, gene mapping, identification of mutations capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences of the invention.

Conditional produce data for this patent did not appear in the printed consorted in the printed consorted in the consorted consorted in electronic format directly from MIPO and the invention in the printed consorted consort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AQLIGLILLMIPGARCESVITQPPSVSGAPGQKVTISCTGSTSNIGGYDL-HWYQQLPGT 63
                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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79.8%; Pred. No. 2.8e-50;
iive 18; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 49652; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March 29, 2003, 09:10:21
Job time : 25.273 secs
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Matches 186; Conservative
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Sequence 9, Applisequence 20, Applisequence 25, Applisequence 23, Applisequence 11, Applisequence 11, Applisequence 29, Applisequence 24, Applisequence 46, Applisequence 46, Applisequence 46, Applisequence 5, Applisequence 6, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Appliance 4, Appliance 50, Appliance 132, Appliance 132, Appliance 4, Appliance 4, Appliance 4, Appliance 6, Appliance 6, Appliance 9, A
                                                                                                                                                                                                                                                                                (without alignments)
6735.375 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 169,
Sequence 3, Ar
Sequence 8, Ar
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1 ATGAGGTCCCCGCTCAGCT......CCCCTACAGAATGTTCATGA 711
                                                                                                                                                                                                                             April 5, 2003, 19:47:34 ; Search time 32.3734 Seconds
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-049-672A-20
US-09-499-672A-250-1
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US-09-152-060-47
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US-08-161-277A-50
US-08-646-981-4
US-08-646-981-4
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US-08-646-53A-4
US-08-65-202-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441362 seqs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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242.4
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                                                                                                                                                                                                                                      Run on:
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Sequence 9, Application US/08487550

Ratent No. 6113898
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION:
TITLE OF INVENTION:
TABLESSEE:
TOTAL
SABBESSEE:
BURNS, DOANE, SWECKER & MATHIS
STREET:
GITY:
Alexandria
                                                                                                       Sequence 13, Appli
Sequence 133, App
Sequence 9, Appli
Sequence 134, Appl
Sequence 123, App
Sequence 123, App
Sequence 121, App
Sequence 121, App
                                Sequence 3, Appli
Sequence 128, App
Sequence 126, App
Sequence 129, App
Sequence 130, App
Sequence 1, Appli
                                                                                                                                                                                                            Sequence 1
Sequence 1
Sequence 2
Sequence 2
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,550

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERRANCY/DOCKET NUMBER: 012712-131

TELEPONE: 703-836-620

TELEPONE: 703-836-620

TELEPAK: 703-836-620

TELEPAK: 703-836-021

INFORMATION POR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 711 base pairs
US-09-240-274-223

US-08-246-093-5

US-09-240-274-123

US-09-240-274-126

US-09-240-274-126

US-09-240-274-129

US-09-240-274-130

US-09-240-274-133

US-09-240-274-134

US-09-240-274-134

US-09-240-274-124

US-09-240-274-124
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LOCATION:
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US-08-487-550-9
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100.0%; Score 711; DB 3; Length 711;

Query Match

N

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                          NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                   FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 650-855-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LIBRARY: ADRETUTO5
; CLONE: 2492122
US-09-049-672A-20
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US-09-049-672A-20

Sequence 20, Application US/09049672A

Parent No. 61359H

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Rarl J.
APPLICANT: Guegler
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Pred. No. 2.4e-187;
; Mismatches 0; Indels
                        0; Mismatches
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STREET: 3174 Porter Drive
CITY: Palo Alto
    100.08;
Best Local Similarity 100.
Matches 711; Conservative
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Length 935;
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Query Match 81.9%; Score 582.6; DB 3; Best Local Similarity 89.8%; Pred. No. 7.8e-152; Matches 637; Conservative 0; Mismatches 69;
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GACCGATTCTCTGGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG 300
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           121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
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                                                   121 ACCTGTGGGGG-----AGACAACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAG 174
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                                                                                              CCAGGAACGGCCCCCAAACTCCTCATGACATTAACAAGCGACCCTCAGGAATTTCT
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Sequence 25, Application US/09049672A

Parent No. 6135941

GENERAL INFORMATION:
APPLICANT: Lall, Preeti
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Baughn, Mariah R.
TILEOP INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCE: 28

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        705
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/049,672A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3174 Porter Drive CITY: Palo Alto
STATE: CA
STATE: CA
STATE: CA
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                              181
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                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
TACCTGAGCCTGACGCCTGAGCAGTGGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 733
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                                                                   TACCTGAGCCTGACGCCTGAGCAGTGCAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
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                                                                                                                                                      CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 709
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Pred. No. 3.6e-140;
0; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.1%;
Matches 612; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION:
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; LOCATION:
US-08-487-550-1
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STREET: 3174 Por
CITY: Palo Alto
STATE: CA
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                                 US-09-049-672A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AGAGGGTCACCATCTCTTGTTCTGGAACCACCTCCAACATCGCAAGTAATTCTGTGCATT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 GGTACCAGCAGCTCCCAGGAACGGCCCCCCAAACTCCTCATCTATGACATTAACAAGCGAC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.6%; Score 530.2; DB 3; Length 895; Best Local Similarity 87.5%; Pred. No. 2.3e-137; Matches 580; Conservative 0; Mismatches 83; Indels 0
               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39.132
REFREENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; CLONE: 3116314
US-09-049-672A-25
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAT 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCACTGGGAGCACCTCCAACATTGGAGGTTAT --- GATCTACATTGGTACCAGCAGCTC 180
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                                                                                                   GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Yr Tom
APPLICANT: Tang, Yr Tom
APPLICANT: We, Henry
APPLICANT: We, Well C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Human Immune system Associated PROTEINS
NUMBER OF SEQUENCES: 28
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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Pred. No. 5.9e-132;
0; Mismatches 104; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSESEGE for Windows Version 2.0
SOFTWARE: FSESEGE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
Sequence 23, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PP-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRA.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: IBM Compatible
DOS
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Best Local Similarity 84.5%;
Matches 599; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: THYRNOT10
CLONE: 2872705
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; Sequence 47, Application US/09152060
; Patent No. 6448230
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                                                                                                                   TTCGGCGGAGGGACCAAGCTGGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT
241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG
                                                   ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA
                                                                                                      TTCGGAGGAGGCCCGGCTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCGGTCACT
                                                                                                                                                       CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACACTGGTGTGTCTCATA
                                                                                                                                                                                                                                                                                                                                                                      CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 709
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APPLICATION NUMBER: US/08/378,939
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
ITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTATION NUMBER: 30, 377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHUNE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                    70.7%; Score 502.6; DB 2; 83.8%; Pred. No. 9.6e-130; ative 0; Mismatches 109;
                                                                                                                                                                                                                       mat_peptide
89..739
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 594; Conservative
                                                                                                                                                                                                                                                                                          sig_peptide
32..86
STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FRATURE:
NAME/KEY: CDS LCCATION: 32.73
FRATURE:
NAME/KEY: MALD:
CCATION: 89..7
FRATURE:
RAME/KEY: 89..7
FRATURE:
CCATION: 32.
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Best Local Similarity
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US-09-152-060-47
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570 ACCACCACACCTCCAAAAGAAAGAACAACAAGAAGGGCCAGCAGCAGCTACCTGAGCCTG 629
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-05-30
EARLIER REPLICATION NUMBER: 60/068, 368
EARLIER REPLING DATE: 1997-05-30
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                                                                                                                                                                                                                                       673 ACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT 709
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Best Local Similarity 80.8
Matches 563; Conservative
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US-09-152-060-29
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US-09-152-060-29
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APPLICATIT. SOED et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PSO03P1. 28
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-50
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EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTING VET: 2.0
SEQ ID NO 47
LENGTH: 885
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Best Local Similarity 80.9%;
Matches 564; Conservative
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CORGANISM: Homo sapiens
US-09-152-060-47
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                                                           GCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTATTCGGAGGAGGG
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APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
2IF: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INVERMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/JOCKET NUMBER: 35,030
REJERMANION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
L'ENGTH: 702 base pairs
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; Sequence 5, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION MARIA
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 TCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAAGGTCACCATCTCG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGGAGGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTG 423
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CRGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: lambda variable and constant domains:
CHROMOSOME/SEGMENT: CE9.1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..702
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..702
UCOATION: 1..702
UCOATION: 1..702
UCOATION: 1..702
UCOATION: 1..702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.9%; Score 468.4; DB 3;
79.9%; Pred. No. 2.5e-120;
iive 0; Mismatches 136;
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Sequence 24, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.;
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 566; Conservative
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404 CTGCCCCCCCCGCTCGTCTCTGTTCCCCCCCTCTCAGGAGCTTCAAGCCAACAAGGCCA
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US-09-152-060-46/c
Sequence 46, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (49)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (78)
OTHER INFORMATION:
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LOCATION: (148)
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APPLICANT: Tang, Y. Tom

APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Budght, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Phare--
STREET.
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                                                                                                                                                                                                                                                                                                                   ZUT: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM:
DOS
SOFTWARE: FESTENG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0497 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CETTORE, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 9,132
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                          STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: LNODNOTO8
CLONE: 3056213
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                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                           JUNEARL INCOMMINION:

JAPPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins.
FILE REFERENCE: PSO03P1.05

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER FILING DATE: 1998-03-12

EARLIER FILING DATE: 1998-03-12

EARLIER FILING DATE: 1997-03-14

EARLIER PEPLICATION NUMBER: 60/040,762

EARLIER PEPLICATION NUMBER: 60/040,710

EARLIER FILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-05

EARLIER FILING DATE: 1997-05-30

EARLIER PEPLICATION NUMBER: 60/048,100

EARLIER PELING DATE: 1997-05-30

EARLIER APPLICATION NUMBER: 60/048,970

EARLIER FILING DATE: 1997-05-05

EARLIER FILING DATE: 1997-05-05

EARLIER FILING DATE: 1997-05-06

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                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: FS 94/10566
FILING DATE: 05-SEP-1994
ATTONEY/AGENT INFORMATION:
NAME: OBLON, NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 22,018
TELEPHONE: 703-413-3000
TELEFRAX: 703-413-3220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "IMMUNOGLOBIN, LIGHT
CHAIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCCTCGGTCACTCTGTTCCCGCCCTCC-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 521; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
58..716
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1..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 58.716
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AACAAGCGACCCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGGCC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTAT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         774 ACCTTGACTATCAGTGGGGCCCAGGTGGAGGATGCGGCTGACTACTACTATTACTCAACA 715
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION:
MUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                      Query Match 57.9%; Score 412; DB 4; Length 928; Best Local Similarity 83.9%; Pred. No. 1e-104; Matches 464; Conservative 18; Mismatches 69; Indels
                                FEATURE:
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (532)
OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-46
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              9
OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                        47 CAGGIGCACGAIGIGAGICIGICCIGACACAGCCGCCCTCAGIGICICIGGGGCCCCAGGGC 106
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                                                                        51;
51.7%; Score 367.4; DB 4; Length 716; 75.2%; Pred. No. 2e-92; tive 0; Mismatches 121; Indels 51.
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575 GCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCC 634
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                                                                93 GCAACAACAACAAGTACGCGGCCAGCAGCTGACCTGAGCCTGACGCTGAGCAGTGCCC 34
153 GGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGCCACCACCACCCTCCAANCAAA
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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83.7%; Pred. No. 1.6e-75;
tive 0; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMINICATION INFORMATION:
TELEPHONE: (206) 622-6930
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
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APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
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SEQUENCE DESCRIPTION: SEQ ID NO: 241:
                                                                                                                                                                                                                                                              Sequence 241, Application US/08991789A
Patent No. 6225054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
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Matches 370; Conservative
                                                                                                                        635 ACAGAAGCTACAG 647
                                                                                                                                                   33 ACAGAAGCTACAG 21
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                                                                                                                                                                                                                       RESULT 14
US-08-991-789A-241/c
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                  437 CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCT 334
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Sequence 268, Application US/09404879A

Patent No. 6468546

GENERAL INRORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 2.10121-462C2
CURRENT PILING DATE: 1999-09-44

NUMBER OF SEQ ID NOS: 393

SEQ ID NO 268

LENGTH: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                           GAGCCGTGACAGTGGCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA
                                                                                                                                                                              CCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGC
                                                                                                                                                                                                         563 ACAAACCCTCCAAACAGGGAACAAGTACGGGGCCAGCAGCAGCTACCTGAGCCTGACGC
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Pred. No. 2.3e-80;
0; Mismatches 47
                                                                                                                                                                                                                                                                                                                                       677 TGGAGAGACAGTGGCCCCTACAGAATGTTCAT 709
                                                                                                                                                                                                                                                                                                                                                                            683 cadadaadacgcigcccigcadaargiicai 715
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LOCATION: (1)...(584)
CTHER INFORMATION: n = A,T,C or G
US-09-404-879A-268
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Best Local Similarity 87.3%;
Matches 378; Conservative
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ORGANISM: Homo sapien
FEATURE:
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299 AGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGG 358
                                       AGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGC---AGCACTCTCG 212
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                                                                                   TATTCGGAGGAGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA
                                                                                                                                                                                           9
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APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
TITLE OF INVENTION: CCMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 771;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FLING DATE: 04-APR-1997
CLASSIFICATION:
ATTONEY/AGENT INFORMATION:
NAME: MAIL, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OO: 22-4900
TELEFRAX: (206) 622-4900
TELEFRAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
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Pred. No. 1.6e-75;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 241, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
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Best Local Similarity 83.7%;
Matches 370; Conservative (
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STATE: Washington
COUNTRY: USA
ZIP: 981.04-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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US-09-062-451-241/c
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                        388 ACCCAGGCAAAGCCCCCCAAATTCATGAGGTTTTATGAGGTTCGGTAATCGGCCTTCAGGGGTTT
                                                                                     328 CTAATCGCTTCTCTGGCTCCAAGTNTGGCAACACGCGCCTCCCTGACCATCTCTGGGCTCC
                                                                                                                                   299 AGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGG
                                                                                                                                                                                                                                                                                                         151 CTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA
179 TCCCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTT
                                                                 CTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCC
                                                                                                                                                                                                       CTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA
                                                                                                                                                                                                                                                                                                                                          TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCA
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This sequence encodes a primatized form of the antibody 7C10 light chain from macaque. This sequence is used in a method which studies new conclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such MAD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune cheticiency virus) or inflammatory disease and tumoures. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; II-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; Mab; macaque; light chain; primate; antigen; CD80;
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TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
                                                                                                                                                                              TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
                                                           GCGGGAGTGGAGCCACCACCCCCCCAACAAAGCAACAACAACAAGTACGCGGCCAGCAGC
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/product= 7C10 light chain
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P-PSDB; AAW63760.
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or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of a primatised form of the light chain of 7C10 antibody.
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                                                                                                                            76.0%; Score 540.2; DB 19; Length 705; 86.1%; Pred. No. 3.2e-128; Live 0; Mismatches 93; Indels 6;
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                                                                                         Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;
                                        production of interleukin-2 (IL-2), T cell prolife antigen-specific immunoglobulin G (IgG) responses.
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P-PSDB; AAW40533.
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                                                                                                                                                                                                                                                                                                                                                                                                     Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
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tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
                                                                                                                                                             'product= "Light chain of 7C10 antibody'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Fig 3a; 89pp; English.
                                                                                                                                                                                                                                                                                                                                      Brams P;
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                                                            Chimeric - Homo sapiens.
Chimeric - Macaca sp.
                                                                                                                                                                                                                                                                                                         (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                    Anderson DR, Hanna N,
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P-PSDB; AAU11538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Antibody HB4CS light chain"
/note= "the start and stop codons are not indicated"
                                                                                                                                                                      241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG
                                                                        301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA
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Antibody light chain; carboxypeptidase; bovine pancreas; cancer; porcine pancreas; radioimminoimaging; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
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/*tag= a
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                                 This cDNA encodes a antibody HB4C5 light chain. This antibody light chain or its fragment is specific for carboxypeptidase from bovine or porcine pancreas and is reactive with human cancer tissue. The antibody light chain and its fragment can be used for preparation of a cancer radioimmunoimaging reagent and therapeutic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                    TATTCGGAGGAGCCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA 418
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                                                                                                                                   75.0%; Score 533.2; DB 19; Length 651; 89.8%; Pred. No. 1.9e-126; ative 0; Mismatches 63; Indels 3;
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         Claim 12; Fig 9; 20pp; Japanese.
                                                                                                                                  Query Match
Best Local Similarity 89.84
Matches 584; Conservative
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Minimum DB E Maximum DB E

Database

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ISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 956)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Ggabba romail inih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov c column: 08

High quality sequence start: 10

High quality sequence stop: 655.
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AGENCOURT 8353826 NIH_MCC_113 Homo sapiens cDNA clone IMAGE:6278335
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JOURNAL
COMMENT
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Result No.

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/db xref="taxon:9606"
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E 1 (Dasses I to 913)

I Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM2476 row: i column: 01

High quality sequence stop: 663.

Location/Qualifiers
AGENCOURT_8351417 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282312
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Pred. No. 4.2e-142;
0; Mismatches 78; I
                                                                          organism="Homo sapiens"
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/organism="Homo sapiens"
/db_xerE="texaon:9606"
/clone_lib="NIH MGC_113"
/clone_lib="NIH MGC_113"
/lab host="Hol10B (phage-resistant)"
/note="Organ: spleen: Vector: pOTB7; Site_1: Xhol; Site_2: RooR1, cDNR made by oligo-dT priming. Directionally cloned into EcoR1/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                AGENCOURT_1976221 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:621484557, mRNA sequence.
BQ708570.
BQ708570.1 GI:21847469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enail: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information as found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2382 row: m column: 22
High quality sequence start: 11
High quality sequence stop: 654.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 894)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                            540
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                                                                                                                                         TACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 660
                                                                                                                                                                                                       TACCTGAGCCTGACGCCTGAGCGAAAGTCCCACAANAGCTACAGCTGCCAGGTCACG 695
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                                                                              AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCCGTCAAG
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                                                          AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG
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                                                                                                                                                                                                                                                                   CATGAAGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTCAT 745
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Matches 598; Conservative

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 819)

NIH-MGC http://mgc.nci.nih.gov/.

Lu Dupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                   CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCA
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                                                                                          AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATT
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BG685644.1 GI:13917041
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/db xref="taxon:9606" |
/clone="IMAGE:6215395" |
/clone="IMAGE:6215395"
                                                                                    873 bp mRNA linear EST 16-JUL-2002
5', mRNA Sequence.
BQ712653.1 GI:21851552
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 TCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCCAGGGCAGAAGGTCACCATCTCG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can by
thtp://imaga.llnl.gov
Http://imaga.llnl.gov
Plate: LLCM384 row: d column: 20
High quality sequence stop: 530.
Location/Qualifiers
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/closue type="primary B-cells from tonsils (cell line)"
/lab_host="Drimary B-cells; Vector: pOTB7; Site_1: XhOI;
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhOI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: Libis is a NIH MCC Library."
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89.3%; Pred. No. 2.8e-139;
ive 0; Mismatches 69;
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/organism="Homo sapiens"
                                          High quality sequence stop: 812.
Location/Qualifiers
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/db xref="taxon:9606"
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/clone="lMAGE:4854290"
/clone="lMAGE:4854290"
/clone="lib="Wilf MGC_48"
/tlssue type="primary B-cells from tonsils (cell line)"
/tlssue type="primary B-cells; ports"
/tlssue cype="primary B-cells; vector: ports", site 1: XhoI;
/note="organ: B-cells; vector: ports", site 1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Galifornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG755185 755 bp mRNA linear EST 15-MAY-2001
6027141114F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854290 5',
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MYH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Insyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1701 row: 1 column: 03
High quality sequence stop: 753.
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                                                                    TTCGGCGGAGGGACCACGTGCTGCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT
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                                             TTCGGAGGAGCCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT
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1007 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6708356 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5749861
EM920020
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Maesa 1 to 1007)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1990)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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Score 555.6; DB 12
Pred. No. 1.8e-138;
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAML2779 row. o column: 14
High quality sequence stop: 712.
High quality sequence stop: 712.
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/note="Organ: ovary (pool of 1); Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGENCOURT 6620012 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590299 BM906351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1060)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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629 TATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 688
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lette://image.lnh.a.G.E. Consortium/LLNL at:
http://image.lnh.gov
Plate: LLAM12364 row g column: 04
High quality sequence stop: 729.
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Post Local Similarity 86.2%; Pred. No. 1.6e-137;
Matches 611; Conservative 0; Mismatches 98; Indels 0;
                                                                                                                                661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT
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/clone="IMAGE:5590299"
/clone_lib="NIH_MGC_125"
/lab_host="DH10B"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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BQ890529
AGENCOURT 8585752 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302538
S, mRNA sequence.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 857)
     Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH MGC Library."
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                                                                                                                             Score 551.6; DB 12; Length 910;
Pred. No. 2.2e-137;
0; Mismatches 74; Indels 5;
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                                                                                                                             77.68;
88.98;
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Matches 631; Conservative
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ORIGIN
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/db_xref="taxon:9606"
/clone="IMAGE-4850330"
/clone=lib="NHH MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
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BG757147 GI:14067800
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1995)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-ramail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCME692 row: p column: 03

High quality sequence stop: 879.

Location/Qualifiers

Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 910)
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                    289 GACCGATTCTCTGGCTCCAAGTCTGACACGTCAGCCACCCTGGGCATCACCGGACTCCAG 348
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                                                                 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA
                                                                                       CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTCTCATA
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AUTHORS
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/clone_lib="NIHMGE:6102538"
/clone_lib="NIHMGE:6102538"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: CoRI; CoNDA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I:M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I:M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
column: 19
High quality sequence stop: 552.
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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77.3%; Score 549.4; DB 14; Length 857;
Best Local Similarity 91.0%; Pred. No. 8.5e-137;
Matches 607; Conservative 0; Mismatches 56; Indels 4;
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/organism="Homo sapiens"
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//db xref="taxon:966"
//clone="nynAge=186574"
//clone="nynAge=186574"
//clone="nynAge=186574"
//clone="nynAge=186574"
//clone="nynAge=186574"
//done=lib="NHH MGC 48"
//done="bype="primary B-cells from tonsils (cell line)"
//db host="DhinB (phage=resistent)"
//note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
//die_"Organ: B-cells; Vector: poTB7; Note: Note: PoTB7; Site_1: XhoI;
//die_"organ: B-cells; Vector: poTB7; Note: Not
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 764)
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rolling. 
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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0; Mismatches 100;
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| Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
| Dasses 1 to 817)
| Millend Institutes of Health, Mammalian Gene Collection (MGC)
| Mational Institutes of Health, Mammalian Gene Collection (MGC)
| Unpublished (1999)
| Contact: Robert Strausberg, Ph.D.
| Email: cgapbs-romail.nih.gov
| Tissue Procurement: Life Technologies, Inc.
| CDNA Library Preparation: Life Technologies, Inc.
| CLONG Library Preparation: Life Technologies, Inc.
| Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
| High quality sequence etop: 817.
| Location/Qualifiers
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/db xref="taxon:9606"
/clone="TMAGE:5224645"
/clone lib="MIH MGC_120"
/lab_host="DH10B"
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BI835917.1 GI:15947467
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BG685967 896 bp mRNA linear EST 01-MAY-2001 602638530F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766335 5', mRNA sequence.
BG685967 GI:13917364
EST.
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size_1.5 kb, insert size range_1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C gruber (Invitrogen). Research Genetics
tracking code_025. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                            188
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/note="Norgan: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: EcoR1: CDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5 adaptor: GGCAGGAG(G): Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 823)

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60265095181 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763148 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                          639 AGCTATCTGAGCCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTC 698
459 ACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCCAACAAGGCCACACACTGGTGTGTCTC 518
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Concact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-ramail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling HonglyRubin Laboratory
CDNA Library Preparation: Ling HonglyRubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
f column: 13
High quality sequence stop: 808.
Location/Qualifiers
                                                                     478 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGGTC
                                                                                                                                              519 ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC
                                                                                                                                                                                                                                                                                        579 AAGGCGGGAGTGGAGACCACCNAACCTCCAAACAAAGAAACAACAAGTACGCGGCCAGC
                                                                                                                                                                                                                       538 AAGGCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGC
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Pred. No. 1.4e-135;
0; Mismatches 57; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:4763148"
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/d_xref="Taxon:9606"
/clone="IMAGE:476635"
/clone="IMAGE:476635"
/clone="IMAGE:476635"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/noce="Organ: B-cells, Vector: pOTB; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: egapba-raminih.bay
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCMAG26 row: k column: 08
High quality sequence stop: 878.
                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 896)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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    /organism="Homo sapiens"

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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1692 row: o column: 20
High quality sequence stop: 841.
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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    .849
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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/clone="IMAGE:4850923"
/clone=lib="NIH MGC 48"
/clone lib="NIH MGC 48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_hoste="Dailmary B-cells from tonsils (cell line)"
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/lab_hoste="Dail"
/inche="Organ: B-cells; Vector: pOTB7; Site 1: Xho!;
Site 2: EcoRl; CDNA made by oligo-dT priming.
Site 2: EcoRl; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xhol sites using the following 5: adaptor: GGACGAGG). Size-selected >SOODp for everage insert size 1.8kb. Library constructed by Ling for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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(without alignments)
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N. JCHOS29 Ggdata/geneseg/genesegn-embl/NA1980.DAT:*

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1 ATGAGGGTCCCCGCTCAGCT......CCCCTACAGAATGTTCATGA 711
                                                                                                                                                                                                              April 5, 2003, 18:12:24; Search time 195.124 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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No.	Score	Match	re Match Length DB I	DB	ai	Description
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7	711	100.0	711	24	AAS17246	DNA sequence of a
٣	709.4	8.66	711	18	AAT62512	Primatised anti-hu
4	582.6	81.9	935	22	AAC66525	Human immune syste
Ŋ	571.4	80.4	884	11	AAQ03609	Sequence encoding
9	565.2	79.5	762	22	AAC84209	Plasmid Glambda-1B
7	558.8	78.6	5679	22	AAC84207	Plasmid Glambda-1A
80	552.6	7.77	768	20	AAX06953	Monoclonal antibod
0	552.6	77.7	768	20	AAX06954	Monoclonal antibod

Anti-HIV-1 recombi DNA encoding novel Primatised anti-hu Macaque primatized DNA sequence of a Antibody HB4C5 lig Human type antihum	Human banign prost Lung cancer relate Human immunne syste Human type antihum Plasmid scPv (CC046 Human type antihum Human type antihum Antibody D lambda	DNA encoding novel Human polymucleoti DNA encoding novel DNA encoding novel Human immune syste Human prostate exp	prostate prostate bladder t ncoding no egions of 04 monkey- ovarian a
AAQ49835 AAS87270 AAY5509 AAV35484 AAS17242 AAV11293 AAV11293	ABK64815 ABK64815 AAC6530 AAH47904 ABL49526 AAH47898 AAC6528 AAC6528	AAS77073 AAK51914 AAS939 AAS93463 AAS93478 AAV2586 ABV2585 AAV343477 AAV34321	ABV22585 ABV28405 AAZ24427 AAS83484 AAN81655 AAT62867 ABQ54438 AAH98186
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## ALIGNMENTS

AAV35488 standard; DNA; 711 BP

RESULT 1 AAV35488

29-SEP-1998 (first entry)

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Monoclonal antibody, Mab, macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idlotype reagent; interleukin-2; IGG; immunoglobulin G;
                                                                                                                                                                                      /*tag= a
/product= 16C10 light chain
                                                     Macaque primatized 16C10 light chain DNA.
                                                                                                                                                               Location/Qualifiers
1..711
                                                                                                                                                                                                                                                                 97WO-US19906
                                                                                                                                                                                                                                                                                      96US-0746361
                                                                                                                     cell proliferation, ss.
                                                                                                                                                                                                                                                                                                          (IDEC-) IDEC PHARM CORP.
                                                                                                                                            Macaca fascicularis.
                                                                                                                                                                                                                                                                 29-OCT-1997;
                                                                                                                                                                                                                                                                                      08-NOV-1996;
                                                                                                                                                                                                                      WO9819706-A1
                                                                                                                                                                                                                                           14-MAY-1998
                                                                                                                                                                 Key
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This sequence encodes a primatized form of the antibody 16C10 light chain from macaque. This sequence is used in a method which studies new moncolonal antibodies (MAD 8) that bind selectively to BT.1 (CD80) or to BT.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoinmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythemators, specific inflammatory bowel disease, allergy and multiple selectoris, graft vs. Inflammatory bowel disease, allergy and multiple selectoris, graft vs. host diseases. B cell lymphoma infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD on be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking BT/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and inhibits production of interleukin-2 (IL-2), T cell proliferation and
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                                                                                                                     New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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                                                                                                                                                                                                                         Example 7; Fig Sa; 87pp; English.
                       Hanna N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 711; Conservative
                   Anderson DR, Brams P,
                                                           WPI; 1998-286601/25.
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                                                                                 P-PSDB; AAW63764.
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Human, macaque monkey, light chain, primatised antibody, 16C10 antibody, neuroprotective, apoptosis inducer; allergy, CD28 receptor antagonist, nel pridgen, CD80, B7.2 antigen, CD86, B cell cancer; metastasis, tumour; B cell lymphoma; B cell leukaemia, autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD86) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7.4 cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or
                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence of a primatised form of the light chain of 16C10 antibody.
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                                  900
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GCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
                     541 GCGGGAGTGGAGACCACCACACACCTCCAAACAAAGAAACAACAAGATACGCGGCCAGCAGC
                                                                       TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
                                                                                                        601 TACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
                                                                                                                                                                                CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "Light chain of 16C10 antibody"
                                                                                                                                             CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                             AAS17246 standard; DNA; 711
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Chimeric - Macaca sp.
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rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the light chain of 16C10, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
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                                                                                                                                                                                                                                                                       Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;
                                                                                                                                                                                                                                                                                                                              ; Score 711; DB 24;
; Pred. No. 8.5e-172;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 711; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DNA sequences (AAT62512 and AAT62513) respectively code for primatised forms (AAW01821 and AAW01822) of the light and heavy chain of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibodis have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
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0
            Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPB). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, cohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, 'osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system associated protein; HISAP-7; immune disorder; infection; autoimmune disease; cancer; ss.
                                                                                      CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA
                                                                                                                                                     GCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
                                                                                                                                                                                                                       TTCGGAGGAGCCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT
                                                                   CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACACTGGTGTCTCATA
                                                                                                                                    AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG
                                                                                                                                                                                                                                                                                                 TACCTGAGCCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system associated protein HISAP-7 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Column 83-84; 54pp; English
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Hillman JL, Au-Young
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P-PSDB; AAB36209.
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Seguence 935 BP; 216 A; 299 C; 248 G; 172 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                             374 GCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTGTGTGGTA
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                                  4 AGGGTCCCCGCTCAGCTCCTGGGCTCCTGCTCTGGCTCCCAGGTGCACGATGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence encoding 4G12 monoclonal antibody (MAb) L chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4G12 MAb; human lung cancer; oesophageal carcinoma; 88.
69
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Score 565.2; DB 22; Length 762;
Pred. No. 1.4e-134;
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91.6%;
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                                                                                                                                                                                                                                                                                                                                                                              AAC84209 standard; DNA; 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence is cloned and synthetic DNA/RNA of human Ab L chain C regions is used as probe to obtain sequences coding for 4G12 MAb.

See also AAQ03607-Q03610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA base sequence coding for 4G12 monoclonal antibody - which specifically with human lung cancer and oesophageal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 884 BP; 219 A; 286 C; 212 G; 166 T; 1 other;
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Matches 623; Conservative
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The invention provides a human monoclonal antibody (I) and its functional fragments specifically reactive with an F protein epitope of respiratory syncytial virus (RSV), and capable of neutralizing infection by the virus such as Glambda-1A or Glambda-1B. The antibody can be expressed by standard recombinant methodology. (I) is useful for detecting RSV by contacting a source suspected of containing RSV with (I) and determining whether (I) binds to the source. (I) is also useful for providing passive immunotherapy prophylactically, to RSV disease in a human. (I) is useful for therapeutic and/or prophylactic treatment of RSV infection in human patients, particularly infants and young children. (I) is also useful as a diagnostic reagent for the determination of RSV mediated disorders or for tracking progress of treatment of the disorders. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human monoclonal antibody and functional fragments, useful for therapeutic and/or prophylactic treatment of respiratory syncytial virus infection, is specifically reactive with the F protein epitope of the virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents the continuous DNA sequence of the coding region of the light chain of plasmid Glambda-1Bpcn.
540
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The invention provides a human monoclonal antibody (I) and its functional fragments specifically reactive with an F protein epitope of respiratory syncytial virus (RSV), and capable of neutralizing infection by the virus such as Glambda-1A or Glambda-1B. The antibody can be expressed by standard recombinant methodology. (I) is useful for detecting RSV by contacting a source suspected of containing RSV with (I) and determining whether (I) binds to the source. (I) is also useful for providing passive immunotherapy prophylactically, to RSV disease in a human. (I) is useful for therapeutic and/or prophylactic treatment of RSV infection in human patients, particularly infants and young children. (I) is also useful as a diagnostic reagent for the determination of RSV mediated disorders or for tracking progress of treatment of the disorders. The present sequence represents the continuous DNA sequence of the expression plasmid clambda-1mAb for the
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78.6%; Score 558.8; DB 22; Length
Best Local Similarity 91.0%; Pred. No. 9.4e-133;
Matches 606; Conservative 0; Mismatches 57; Indels
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                                                     (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                    Taylor G;
                                                                                                                                                                                                                                                         WPI; 2001-024947/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the DNA sequence of a polymucleotide that encodes the light chain variable region (see AAW88465) of the recombinant human monoclonal antibody (MAD) 4BS. 4BS recognises antibodies specific for GD2 antigon antibodies. Antibodies specific for GD2 recognise various cancers including glioblastoma, neuroblastoma, malignant and/or metastatic melanoma, breast adenocarcinoma, malignant adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and prostate adenocarcinoma. The invention encompasses 4BS derivatives with immunologic specificity for antibodies specific for GD2. These derivatives, or antigon binding fragments, comprise regions of the 4BS VD junction and regions spanning the 4BS CDRs. Other derivatives include Fab, F(ab')2, Fab', scfv and isolated heavy and ight chains. Polymucleotide fragments (see AAX06951-54), both coding and complementary strands, encoding 4BS antibody V regions are also provided, as well as therapeutic plasmids and vectors, including vaccinia virus vectors, comprising these polymucleotides. He has been shown to mimic GD2, and is particularly useful in generating a host immune response to cancer. Products of the invention can be used in the detection and treatment of e.g.
ACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAAAT 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylactic therapy to reduce risk of recurrence
                                       ACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAAT
                                                                                                                                                                                                                                                                                            Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm; diagnosis; therapy; melanoma; neuroblastoma; garcoma; lung carcinoma; metastasis; anti-idiotype antibody;
                                                                                                                                                                                                                                                                 Monoclonal antibody 4B5 light chain variable region DNA
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                     AAX06953 standard; DNA; 768 BP
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                        primitive neural ectodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and large cell lung adenocarcinomas, gruamous cell carcinoma, bronchoalveoarcarcinoma, epithelial adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular adenocarcinoma, squamous and adenocarcinomas of the uterine cervix, uterine and ovarian
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                                                                                                                                                                            epithelial carcinoma, prostatic adenocarcinoma, transitional squamous cell carcinoma of the bladder, B and T cell lymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia, malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
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                                                                                                                                                                                                                                                                                                                                                                 77.7%; Score 552.6; DB 20; Length 768; 89.6%; Pred. No. 2.2e-131;
astrocytoma, oligodendroglioma, ependymoma, medulloblastoma
                                                                                                                                                                                                                                                                                                                   Sequence 768 BP; 169 A; 256 C; 202 G; 141 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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AAX06954/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the complementary strand of a DNA sequence (see also
AAX06953) that encodes the light chain variable region (see AAW089465)
of the recombinant human monoclonal antibody (MAB) 485.

of the recombinant human monoclonal antibody (MAB) 485.

crecomises antibodies specific for GD2 antigen antibodies. Such
antibodies recognise various cancers including glioblastoma,
concompasses abs derivatives mail cell lung carcinoma,
colon adenocarcinoma and prostate adenocarcinoma. The invention
encompasses 485 derivatives with immunologic specificity for
antibodies specific for GD2. These derivatives, or antigen binding
fragments, may comprise regions of the 485 VDJ junction and regions
spanning the 485 CDRs. Other derivatives include Reb, F(ab') 2,
confidents apecific for GD2.

fragments (see AAX06951-54), both coding and complementary strands,
encoding 485 antibody V regions are also provided, as well as
encoding 485 antibody V regions are also provided, as well as
encoding 485 antibody V regions are also provided, as well as
encoding 485 antibody V regions are also provided, as well as
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encoding 485 antibody V regions are also provided, as well as
encoding 485 antibody V regions are also provided, as well as
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generating a host immune response to cancer. Products of the
gramman encoding 480 and vectors, including virus vectors,
primitive neural ectodermal tumour (PNET), pancreatic ductal
adenocarcinoma, small and large cell lung adenocarcinomas
endenocarcinoma, small and large cell lung adenocarcinoma, such as ductal and lobular adenocarcinoma, cell carcinoma of the uterine cervix, uterine and ovarian
epithelial carcinoma of the bladder, B and T cell lymphoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylactic therapy to reduce risk of recurrence
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0
                                                             Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma; asrcoma; lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.7%; Score 552.6; DB 20; Length 768; 89.6%; Pred. No. 2.2e-131; ive 0; Mismatches 69; Indels 0;
                                Monoclonal antibody 4B5 light chain variable region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 768 BP; 141 A; 202 C; 256 G; 169 T; 0 other;
                                                                                                                                                                             Location/Qualifiers complement (43..750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 80; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                             (NOVO-) NOVOPHARM BIOTECH INC
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(first entry)
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Matches 594; Conservative
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                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody; HIV-neutralising monoclonal antibody; immunoglobulin; AIDS; acquired immune deficiency syndrome; chimeric antibody; surface glycoprotein gpl20; V3 loop; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 ACGCGCCAGCAGCTACCTGAGCCTGACCCTGAGCAGTGGAAGTCCCACAGAAGTACA
647 AGAGGGTCACCATCTTGTTCTGGAAGCAACTCCAACATCGGAAGTAAGACT
                                                                                                                                                                                                CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCA
                                                                                                                                                                                                                                                                                                 527 CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCA
                                                                                                                                                                                                                                                                                                                                                                    287 TCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCC
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                                                                       107 AGAAGGTCACCATCTCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATT
                                                                                                                                                                      167 GGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGAC
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/note= "encodes recombinantly modified 447-52D
light chain"
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Seguence 810 BP; 176 A; 275 C; 211 G; 148 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                         EBV-transformed cell lines and mouse-human heterohybridomas producing human MAbs specific for the gp120 V3 loop of HIV-1 MN isolate were obtained. MAb 447-52D was found to recognise the tetrapeptide motif GPGR, i.e. the Principal Neutralising Determinant common to the V3 loop of different HIV isolates. A recombinant Ab was produced in which the L chain V region was derived from 447-52D and to which a signal sequence and a L chain intronic sequence are appended, fused to a fragment contg. a short intronic segment of the human lambda 2 C region and the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTCGGAGGAGCCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCA
                                                                                                                                                                                        neutralising activity preventing or treating
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m
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                                                                                                                                Pfarr DS
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 654 BP; 156 A; 199 C; 178 G; 121 T; 0 other;
                                                                                                                                Mark GE,
                                                                                                                                                                                         HIV
                                                                                                                                                                                        recombinant human antibody - with inst at least two isolates, useful
                                                                                                                                Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                         lambda 2 constant encoding domain.
                                                                                                                                                                                                                                      Example 9; Fig 2B; 154pp; English
                                                                                                                                                                                                                 infection in diagnosis, etc.
                                                         92US-0861701.
                                  93WO-US02629
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarry
Matches 593; Conservative
                                                                               (MERI ) MERCK & CO INC.
(JOHN/) JOHNSON L S.
(PFAR/) PFARR D S.
                                                                                                                                Conley AJ, Emini EA,
                                                                                                                                                     WPI; 1993-336600/42.
                                                                                                                                                                  P-PSDB; AAR42163
                                  23-MAR-1993;
                                                         01-APR-1992;
         14-0CT-1993
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (III) sequences. (I) primers, oligomers, and for chromosome and precombinant production of (II). The companies are also used in diagnostics as expressed sequence tags to ridentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating classing aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in the produce of the produce of the consider of the remaining classics, forensics, gene mapping, identification of mutations and to produce the transfer of assess by bodiversity and to produce the transfer of assess buddiversity and to produce the transfer of assess buddiversity.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
482 AGGCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                          CGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 652
                                                                                                                                                                                                                                                                          CGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #23074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
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   DB 23; Length 810;
                                                          73; Indels
76.8%; Score 546.2; DB 2:
89.0%; Pred. No. 9.7e-130
iive 0; Mismatches 73.
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Chimeric Homo sapiens.
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                     Best Local Similarity 89.0 Matches 590; Conservative
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FEATURE:
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Sequence 9, Al
Sequence 20,
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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                                   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-379-072A-20
US-08-481-869-20
US-08-481-869-20
US-08-476-237-16
US-08-476-237-16
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US-09-025-769B-169
US-08-634-783A-4
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US-08-761-277A-50
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US-09-404-879A-268
US-08-991-789A-241
US-09-062-451-241
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US-08-078-93-11
US-09-049-672A-25
US-09-049-672A-23
US-09-152-060-47
US-09-152-060-29
US-09-152-060-46
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Maximum Match 100%
Listing first 45 summaries
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US-08-487-550-1

| Sequence 1, Application US/08487550 |
| Sequence 1, Application US/08487550 |
| Patent No. 6113898 |
| APPLICANT: Anderson, Darrell R. |
| TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC |
| TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS |
| TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS |
| TITLE OF INVENTION: IMMINOSUPPRESANTS" |
| NUMBER OF SEQUENCES: 12 |
| CORRESPONDENCE ADDRESS: ADDRESSE: BURNS, DOANE, SWECKER & MATHIS |
| STREET: 699 Prince Street |
| COUNTRY: USA |
| COUNTRY: USA |
| COUNTRY: USA |
| CALLE OF INVENTION |
| COUNTRY: USA |
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: US/08/487,550
FILING DATE: US/03/1995
CLASSIFICATION: 435
ATTONENTY/AGENT INFORMATION:
NAME: TESKIN RObin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
TELERBENCE/DOCKET NUMBER: 012712-131
TELEBRENCE/DOCKET NUMBER: 012712-131
TELEBRENCE/DOCKET NUMBER: 012712-131
TELEBRENCE/DOCKET NUMBER: 012712-131
US-08-477-553A-44
US-08-259-372A-9
US-08-468-671-9
US-08-345-321-7
US-08-345-321-7
US-08-36-125-10
US-08-36-125-10
US-08-136-125-10
US-09-107-628-10
US-09-107-628-10
US-09-107-628-10
US-09-108-10
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US-09-108-10
US-09-108-10
US-09-260-527-4
US-09-260-527-4
US-09-260-527-4
US-09-079-029-6
US-09-079-029-7
US-08-259-372A-15
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GCCCCTGTGCTGGTCATCTATGCTGACAGCGAACGGCCCTCAGGGATCCCTGCGCGCATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lambda variable and constant domains CE9.1
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET NUMBER: 35,030
REFERENCE/POCKET NUMBER: 35,030
REFERENCE/POCKET NUMBER: 35,030
RELEPAX: 703-836-620
TELEPAX: 703-836-620
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHRARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME: lambda Harden and Constant A
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CHROMOSOME/SEGMENT:
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LOCATION:
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LOCATION:
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                                     Gaps
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Sequence 5, Application US/08523894

PAPLICANT: Hanna, Nabil

APPLICANT: Newman, Roland A. APPLICANT: Newman, Roland A. APPLICANT: Reff Mitchell E. TITLE OF INVENTION: Therapy

NUMBER OF SEQUENCES: 59

CORRESSONDENCE ADDRESS: ADDRESS: ADDRESSE: BURNS, DOANE, SWECKER & MATHIS

STREET: 49 Prince Street

STREET: VA
                                                                                                             1 ATGAGGGTCCCCGGTCAGGTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCAGGTGT
                                                                                  1 ATGAGGGTCCCCGCTCAGCTCCTGGGCCTCCTGCTCTGCTCCCAGGTCCAGGTGCACGATGT
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              Pred. No. 3.4e-186;
100.0%; Prea. ....
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: , IBM PC compatible
       Best Local Similarity 100.
Matches 705; Conservative
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                          121 ACCTGTGGGGG-----AGACAACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAG 174
                                                             121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: O'CLEAY, Neal C.
APPLICANT: Corleay, Neal C.
APPLICANT: Gradeler, Neal C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES. 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
STATE: CA
COUNTY: USA
                                                                                                   CCAGCGCGCCCCTATACTGGTCATCTATGATAGTGACCGGCCCTCAGGGATCCCT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                        Sequence 9, Application US/08487550

Betent No. 6113898

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Frince Street
CITY: Alexandria
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                                                                                                             601 crdacccrrdaccarccaaacrccacadaacracacrcccacaccaccarcarcarcaaggg 660
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GAGACCACCACCACCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGCTACCTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIA, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          664 AGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
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TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.1
Matches 612; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , NAME/KEY:
, LOCATION:
US-08-487-550-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                  RESULT 3
US-08-487-550-9
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PRIOR APPLICATION DATA:

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124 TGTGGGGGAGACAACAGT-----AGAAATGAATATGTCCACTGGTACCAGCAGAAG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 rerececreacicadecrecerecerereresererecereseacadeses da 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0%; Pred. No. 1.7e-117;
Matches 567; Conservative 0; Mismatches 130;
                                                   Sequence 11, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVARIENCE: RODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ STREET: 555 THIRTEENTH ST. N.W. CITY: WASHINGTON STATE: D. C. COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6041
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 902 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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89..739
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32..86
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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FEATURE:
NAME/KEY: CDS
LOCATION: 32...
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : LOCATION:
US-08-378-939-11
                 RESULT 5
US-08-378-939-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.1%; Score 473; DB 3; Length 93
80.4%; Pred. No. 6.5e-122;
tive 0; Mismatches 130; Indels
            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CETTON, Michael C
REGISTRATION NUMBER: 39.132
REFERENCE/DOCKET NUMBER: PF-0.
TELECHMANICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 80.4 Matches 570; Conservative
                                                                                                                                                                                                                                                                                                                                        ; IMMEDIATE SOURCE:
; LIBRARY: ADRETUTOS
; CLONE: 2492122
US-09-049-672A-20
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                          212 CCAGGCAAAGCCCCCAAAATCATGATTATGAGGTCAGTAAGCGGCCCTCAGGGGTTTCT 271
                                                                        272 AATGGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAG 331
                                                                                                           GCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGGACAGGGCTAGTGATCATCCGGTC 354
                                                                                                                                                               TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCGAAGGCTGCCCCCCCGGTCACT 414
                                                                                                                                                                                                                                                                                                                                                                                   TACCTGAGCCTGACGCCTGAGCAGTGCCCACAGAAGCTACAGGTGCCAGGTCACG 654
175 CCAGGGGGGCCCCTATACTGGTCATCTATGATAGTGACGGGCCCTCAGGGATCCCT
                                                       GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAG
                                                                                                                                                                                                                    CTGTTCCCGCCTCCTCTGAGGGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA
                                                                                                                                                                                                                                  AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG
                                                                                                                                                                                                                                                                                                                            GCGGGAGTGGAGACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hallman, Jennier L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Vue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN INMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCES: 18
ADDRESSEE: Incycle Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                       655 CATGAAGGGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT 703
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ZIT: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FastSEC for Windows Version 2.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
MAME: CETTONE, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Drive COUNTRY: no. 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 25, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-049-672A-25
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124 TGTGGGGGAGA-----CAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCA 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GCGCGGCCCCTATACTGGTCATCTATGATAGTGACCGGCCCTCAGGGATCCCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 GGAGCGGCCCCAAACTCCTCATCTATGCTAATGATCAGCGTGCCTCCGGGGTCCCTGAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 CGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 CGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGGCCC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 GGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     64.7%; Score 456; DB 3; Length 89
82.8%; Pred. No. 3.3e-117;
ive 0; Mismatches 105; Indels
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                                            S
REPERENCE/DOCKET NUMBER: 39,132
REPERENCE/DOCKET NUMBER: PF-0497 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4166
TELEFAX: 650-845-4166
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Sequence 23, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.;
APPLICANT: Lal, Preeti
                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHRACATERISTICS:
LENGTH: 895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 82.8 Matches 535; Conservative
                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: LUNGTUT13
; CLONE: 3116314
US-09-049-672A-25
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CTGTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACAGGTGTGTCTCATA 474
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                                                                                                                                                                                                                                                                                 511 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG 570
                                                                                                                                                                                                                                                                                                                                                             535 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC 594
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                                  TTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACT 414
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Pred. No. 1.5e-111;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE OF INVENTION: 28 Human Secreted Proteins
FILE OF INVENTION: 28 Human Secreted Proteins
FILE OF INVENTION: 28 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER APPLICATION NUMBER: 60/040,100
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER PELING DATE: 1997-05-30
EARLIER PELING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-07-10-19
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US-09-152-060-47
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Best Local Similarity
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US-09-152-060-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 reriececróakérelőkécéredérérérésérérelősérérelősákérelősarelenérele 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 riceacresaaccascascaresaresaresaratraraacraristrocresaraccaacascas 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGGACAGGGCTAGTGATCATCCGGTC 354
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                                                                                               APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.6%; Score 455.4; DB 3; Length 79.8%; Pred. No. 4.8e-117; tive 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
ATHOR DATE:
ATHOR DATE:
ATHORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0497 US
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMINICATION INFORMATION:
TELEPHONE: 650-855-0555
Tang, Y. Tom
Yue, Henry
Au-Young, Janice
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 891 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 566; Conservative
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; CLONE: 2872705
US-09-049-672A-23
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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                             APPLICANT:
APPLICANT:
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184 GCCCCTATACTGGTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTC 243
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                                                                                                                                                                                                                                                                                                                                                                    CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGG 663
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                                                                                                                                                               244 TCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
                                                                                                                                                                                                                                                       GAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCGGGTCTTCGGAGGA 363
                                                                                                                                                                                                                                                                                                327 daddcirakiratiacidccadcarardacadcarccccccagrirgargricdccda 386
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APPLICANT: ROSEN et al.

TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P5703P1, 12

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER FILING DATE: 1998-09-11

EARLIER FILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-14

EARLIER APPLICATION NUMBER: 60/040,762

EARLIER APPLICATION NUMBER: 60/040,703

EARLIER APPLICATION NUMBER: 60/040,710

EARLIER FILING DATE: 1997-03-14

EARLIER APPLICATION NUMBER: 60/048,100

EARLIER APPLICATION NUMBER: 60/048,100

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER RILING DATE: 1997-05-30

EARLIER RILING DATE: 1997-05-30

EARLIER RILING DATE: 1997-06-30

EARLIER RILING DATE: 1997-06-30

EARLIER FILING DATE: 1997-06-30

EARLIER FILING DATE: 1997-06-30

EARLIER FILING DATE: 1997-12-19

NUMBER: OF SEO ID NOS: 118

SOFTWARE: PATENTIN VOLUMER: 50/048,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.09-152-060-29
Sequence 29, Application US/09152060
Patent No. 6448230
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                                                                                                                                                                                                                                                                                                                                                     184 GCCCCTATACTGGTCATCTATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTC 243
                                                                                                                                                                                                                                                                                                                                                                              199 CCTCCCAAACTCCTGTCCTACAGGAATAATAACCGGCCCTCAGGGGATCTCAGAGAGATTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                              363
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                                                                                                                                                                                                                          79 chdachcadccccccrcddrichccaaddachraadacadccdccacrcachdcacrcacc 138
                                                                                                                                                                                                                                                                     130 GGAGACAACAGTAGAAATG----AATATGTCCACTGGTACCAGCAGAGAAGCCAGCGCGG 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC
                                                                                                  61.6%; Score 434; DB 4; Length 879;
81.1%; Pred. No. 4e-111;
cive 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    679 AGCACCGTGGAGAAGACGGTGGCCCCTACAGAATGTTCAT 718
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TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003D1.US
FILE REFERENCE: PZ003D1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1999-09-11
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER APPLICATION NUMBER: 60/040,703
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
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EARLIER FILING DATE: 1997-03-14
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Patent No. 6448230
GENERAL INFORMATION:
                                                                                                                                            Matches 519; Conservative
                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-29
                                                                                                                      Local Similarity
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US-09-152-060-46/c
LENGTH: 879
                                                                                                    Query Match
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                                                      GTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGT 683
                                                                                 66 TGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCCAGGACAGACGGCCAGGATCACCTG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
ITILE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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81.0%; Pred. No. 9.8e-109;
live 0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIPECATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER: SPINS
REGISTRATION NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Hillman, Jennifer L.
Lal, Preeti
Tang, Y. Tom
Yue, Henry
                                                                                                                                                                                       361 GGCCCTACAGAATGTTCAT 342
                                                                                                                                                          684 GGCCCCTACAGAATGTTCAT 703
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 81.09
Matches 524; Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-4166
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; LIBRARY: LNODNOTO8
; CLONE: 3056213
US-09-049-672A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900 AAGAAATATGTWTATTGGTACCAMCAGAAGTCAGGCCCAGGCCCCTGTGCTGCTGTCTA 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 TGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGGAA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               840 TGAGGACAACAAAAGACCCTCC-GGATCCCTSAGAGATTCTYTGGCTCCAGYTCAGGGAC 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 CACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTGACTATTACTGTCA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 AGTGGCCACCTTGACTATCAGTGGGCCCCAGGTGGAGGATGCGGCTGACTACTGTTA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 GGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGAGGGACCCGGGTGACCGTCCT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 AGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTTCA 443
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EARLIER FILING DATE: 1997-05-30
EARLIER PEPLICATION NUMBER: 60/048,357
EARLIER PILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER PELING DATE: 1997-12-19
NUMBER: OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE

LOCATION: (532)

OTHER INFORMATION: n equals a,t,g, or c
08-09-152-060-46
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OTHER INFORMATION: n equals a,t,g,
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INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                       PE: DNA
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364
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                                                                                                                                                                                                                                                                                                                        597 CCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCA 656
                                                                                         237 GCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACGATCAACGGGGTCGAGGC
                                     177 AGCGCGGCCCCTATACTGGTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGA
                                                                                                       305 TCGCTTCTCTGGCTCCATCGTTGGGAACAAAGCCGGCCTCACCATCACGGGGGCCCAGGC
                                                                                                                                           297 CGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGGACTAGGGGCTAGTGATCATCCGGTCTT
                                                                                                                                                               365 AGATGATGAATCTGATTATTGT---GTCCTATATAGGCGTAGTGGCTCTTGGGTGTT
                                                                                                                                                                                                CGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCGGTCACTCT
                                                                                                                                                                                                                  GTTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAG
                                                                                                                                                                                                                                                                    TGACTICTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC
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Sequence 5, Application US/08793450

Sequence 5, Application US/08793450

GENERAL INFORMATION:

APPLICANT: BDELMAN, LENA
APPLICANT: KACZOREK, MICHEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABHIH, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CONTY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450 FILING DATE: 03-MAR-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
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107 AGACGGCCAGGATCACCTGTGGGGGAGACAGTAGAAATGAGAATATGTCCACTGGTACC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 AGCAGAAGCCAGCGCGCGCCCTATACTGGTCATCTATGATGATGAGGGGCCCTCAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 AGCAGAAGCCAGGACAGCACCTGTACTTGTCTATGGTAAAAACAACGGGCCCTCAG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 GGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 GGAAGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 CAGGIGCACGAIGIGCCIAIGAACIGACICAGCCACCCICGGIGICAGIGICCCCAGGAC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 cAGGTGTCCACTCCGACATCGAGCTCACGACCCTGCTGTGTGTCTGTGCCTTTGGGAC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AGACAGTCAGGATCACATGCCAAGGAGACGCTCAGAACCTATTATGCAAGCTGGTACC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 GGGTCGAGGCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 AGCTTCAAGCCAACAAGACCACACTGTGTGTCTCATAAGTGACTTCTACCGGGAGCCG 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 ATCCGGTCTTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617 AGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.8%; Score 407.4; DB 4; Length 716; Best Local Similarity 78.0%; Pred. No. 8.7e-104; Matches 536; Conservative 0; Mismatches 106; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "IMMUNOGLOBIN, LIGHT
CHAIN"
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMUNICATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOUSCULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: CDS
                                                                                                              INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 716 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: sig_peptide
LOCATION: 1..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
58..716
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COTHER INFORMATION:
US-08-793-450-5
                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..716
FEATURE:
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NAME/KEY:
LOCATION:
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGCCACACTGGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 ACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAAATCAGGG-----AACACCGC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 CACCCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTGACTATTACTGTCAGGTGTG 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 CAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570 CAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCA 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 GAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCTCCAANCAAAG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Gaps
                                                                                                                   Sequence 268, Application US/09404879A

Sequence 268, Application US/09404879A

GENERAL INCOMMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 268

LENGTH: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 GCCCAAGGCTGCCCCCTCGGTCACTCTTCCCACCCTCCTGAGGAGCAAAAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 GGACAGGGCTAGTGATCATCCGGTCTTCGGAGGAGGGACCCGGGTGACCGTCCTAGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
43.5%; Score 306.6; DB 4;
Best Local Similarity 85.0%; Pred. No. 6.7e-76;
Matches 367; Conservative 0; Mismatches 57;
677 AGACAGTGGCCCCTACAGAATGTTCAT 703
                               689 AGACGGTGGCCCTGCAGAATGTTCAT 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(584)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      630 CAGAAGCTACAG 641
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 CAGAAGCTACAG 21
                                                                                         RESULT 13
US-09-404-879A-268/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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US-08-991-789A-241/c ; Sequence 241, Application US/08991789A ; Patent No. 6225054 ; GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGGTCTTCGGAGGAGGGACCC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 ATTATTACTG---CAGCTCATATACAAGCAGCAGCACTCTCGTGTTTGGCGGAGGGACCA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCCCACCCTCCT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 éreacerregregrahahahahdictennegraceacaceceaeseasececea 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AATTCATGATTTATGAGGTCGGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       creaseascricaaeccaacaaeseccacacrescresrerearaaereacriciaece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 GGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 TACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT
APPLICANT: Frugars, ...
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 771;
                                                                                                                                                                                                                                                                                                                                           NAME: POCTER, Jame E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPRA: (206) 632-6031
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.8%; Score 273.2; DB 4
79.2%; Pred. No. 1.3e-66;
tive 0; Mismatches 85
                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
;
SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-991-789A-241
                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                             CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 336; Conserv
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371 GGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCCCGCCCTCGT 430
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                                                                                                                                                                                                                                                                           Sequence 241, Application US/09062451
| Sequence 241, Application US/09062451
| Patent No. 6344560
| GENERAL INFORMATION:
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| APPLICANT: Smith, John M. |
| TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER INTERSPONDENCES. 297 |
| CORRESPONDENCES. 297 |
| ADDRESSEE: SEED and BERRY LLP |
| STREET: 6300 Columbia Center, 701 Fifth Avenue |
| CITY: Seattle |
| CITY: Seattle |
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 210121.419C2
TERFENCE/DOCKET NUMBER: 210121.419C2
TERFENCE/DOCKET NUMBER: 210121.419C2
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
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US-09-062-451-241
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US-09-062-451-241/c
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1 ATGAGGGTCCCCGCTCAGCT......CCCCTACAGAATGTTCATGA
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AB064143 Homo sapi AB064148 Homo sapi AB064149 Homo sapi AB064149 Homo sapi AB064149 Homo sapi AB0641219 Homo sapi AB0641219 Homo sapi AB0641219 Homo sapi AB064120 Homo sapi AB06426 Homo sapi AB06426 Homo sapi AB064169 Homo sapi AB064169 Homo sapi AB064169 Homo sapi AB064110 Homo sapi AB064110 Homo sapi AB064111 Homo sapi AB064111 Homo sapi AB064211 Homo sapi AB064224 Homo sapi AB064224 Homo sapi AB064224 Homo sapi AB064224 Homo sapi AB064224 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AB064229 Homo sapi AR108866 Sequence AR135362 Sequence AB064208 Homo sapi X14583 Human mRNA Homo sapi Homo sapi Homo sapi Homo sapi sapi sapi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Homo BC012876 F AF191795 F AB064228 F AR108862 S AB064142 F SUMMARIES AB064148 AB064147 AB064219 HSIGVL027 HSIGVL006 AB064141 AB064227 AB064172 AB064206 AB064226 HSIGVL021 AB064150 AB064169 HSIGVL025 AB064178 AR108866 AR135362 AB064208 HSIGLV BC020233 AB064143 AB064188 BC022098 AB064149 AB064166 AB064203 AB064171 AB064170 AB064151 AB064216 AB064222 AB064218 AX287808 AB064205 DB Length Query 582.6 575.4 575.4 575.4 575.4 576.6 566.6 566.4 562.8 562.8 562.8 558 558 557.6 556.4 Score 548.4 547.8 546.2 546.2 545.6 548.4 Result

ALIGNMENTS

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Sequence

540.4 540.2 538.8 534.8

PAT 14-FEB-2001 1 (Dases I to 711)
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.
Human Br. 1.-specific primatized antibodies and transfectomas
expressing said antibodies
Patent: US 6113898-A 9 05-SEP-2000; linear DNA 711 bp Sequence 9 from patent US 6113898. AR108866 AR108866.1 GI:12825142 Unknown. Unclassified. Unknown. RESULT 1
AR108866
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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790 bp mRNA linear PRI 02-JUL-2002
Hemo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
AB064208
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                             81.9%; Score 582.6; DB 6;
89.8%; Pred. No. 1.1e-140;
cive 0; Mismatches 69;
Patent: US 6135941-A 20 24-OCT-2000;
Location/Qualifiers
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                                                               /organism="unknown"
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637; Conservative
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.1 (bases 1 to 935)
Hillman, J.L., Lal, P., Tang, Y. Tom., Yue, H., Au-Young, J.,
Corley, N.C., Guegler, K.J. and Baughn, M.R.
Human immune system associated molecules
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Sequence 20 from patent US 6135941.
AR135362
                                                                     132
      Location/Qualifiers
                                             /organism="unknown"
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/product="immunoglobulin lambda light chain VLJ region"
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SCQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVN"
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Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.

Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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                                                                                                                                          Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toycake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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Pred. No. 8.3e-139;
0; Mismatches 36;
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    . 790
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /clone="L68"

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/gene="IGL"
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PRI 27-NOV-1995
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SNICANNYVSWAQDLBGTAPKLLIYDNKRPBGSIPDRFSGSKSGTSATLGTGTGTGTG
EADYYCGTWDSSLAGAVFGGGTKLTVLGQPFKAAPSVTLFPPSSEELQANKATLVCLIS
DFYPGAVTVAWKADSSPVKAGVBTTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kishimoto, T., Okajima, H., Okumoto, T. and Taniguchi, M. Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells (11), 4385 (1989)
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Submitted (03-MAR-1989) Kishimoto T., Yoshitomi Pharmaceutical
Industries Ltd, Research Labs, 7-25 Koyata 3-chome, Iruma Shi,
Saitama, 358 Japan
2 (bases 1 to 414)
                                                                                                547
                                                                                                                                                                               608 GCTACCTGAGCCTGACCCTGAGCAGTGGAAGTCCCACAAAAGCTACAGCTGCCAGGTCA 667
428 CTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCA 487
                                               TAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCA
                                                                                                488 TANGTGACTICTACCCGGGAGCCGIGACAGIGGCCTGGAAGGCAGAIAGCAGCCCCGTCA
                                                                                                                                                  539 AGGCGGGAGTGGAGACCACCACACCTCCAAACAAAGCAACAAGTACGCGGCCCAGCA
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/product==lambda-chain precursor (AA -20 to 215)"
/protein_id=="CAA33725.1"
/db_xref="GI:33395"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 870)
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                                                                                                                                                                                                                                                                                                                                                                                 CGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC 716
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Data kindly reviewed (03-JUL-1989) by Kishimoto
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/tissue_type="lymph node"
25. .732
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/cell_line="4612"
/cell_time="4612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mRNA for Ig lambda-chain. X14583.1 GI:33394
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/note="C re
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415. .729
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Homo sapiens
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Query Match Best Local

유 ò g ò 임 8 g ઠે 음 ò 셤 ò g ò 셤 ò

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/procein_id="AAH2023.1"
/db_xref="G1:18044241"
/db_xref="G1:18044241"
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ISDFYPGAVTVAMKADSSPYKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: h Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                             Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiso, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCT---CAG
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                    Tissue Procurement: Louis Staudt cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
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/codon_start=1
/product="Unknown (protein for MGC:31936)"
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Pred. No. 1e-137;
0; Mismatches 68; Indels
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/clone="MGC:31936 IMAGE:4765518"
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
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293 c 227 g
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Email: cgapbs-r@mail.nih.gov
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Best Local Similarity 89.6%;
Matches 638; Conservative
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Submitted (19-DBC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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        Length 870;
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                                                                                85; Indels
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Contaçt: MGC help desk
    Score 573; DB 9; I
Pred. No. 3.5e-138;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC020233.1 GI:18044240
                                            88.0%;
            80.68;
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Mammalia; Eutheria;
1 (bases 1 to 903)
                                        Best Local Similarity ....
Matches 624; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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800 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
AB064188
       CLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSY
SCQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGGGSGGGS
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Catarrhini; Hominidae; Homo.
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Homo sapiens
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                                                                                                                                                              Score 570.6; DB 9;
Pred. No. 1.5e-137;
0; Mismatches 39;
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/gene="IGL"
/note="pelB signal peptide"
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Mammalia; Eutheria; Primates;
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TGSSSNIGAGYDVHWYQQLPGTAPKLLIYGDINRPSGVPDRRSGSKSGTSASLAITGL
QAEDEADYYCQSYDSSLSGSVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLV
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="BAC01771.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              827 bp mRNA linear PRI 02-JUL-;
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
Region, partial cds, clone:L3.
     417
                    514
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                                                                                                                                                                                                        AAGGCGGGAGTGGAGCCACCACCCTCCAAACAAAGCAACAAGTACGCGGCCAGC 597
                                                                                                                                                                                                                                                                            AGCTACCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTC 657
                                                                   ACTCTGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTC 477
                                                                                                                                                                             574
                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="Lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
GTATTCGGAGGAGGCGCCGGCTGACGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCGGTC
                                                                                                                                                         ATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
                                                                                                                                                                                                                                                                                                                                                                   ACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 709
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URL:http://www.fujita-hu.ac.jp/immunity/
Location/Qualifiers
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/gene="IGL"
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Kurosawa, Y.
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TGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSAGLAITGL
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CLISDPYPGAYTVARALDSSPYKAGYETTTPEKQGNKYAASSYLSITPEQWKSHKSY
SCQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGG"
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                Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/prodon="immunoglobulin lambda light chain VLJ region"
/protein_id="BACO1816.1"
/db_xref="G1:21669583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TOTCCTGACACACCCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCTCGTG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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                                                                                                                           Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(Email:Kurosawa@tujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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Pred. No. 1.6e-136;
0; Mismatches 39;
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256 c 217 g 151 t
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1. 800

Organism="Homo sapiens"

/db xref="taxon:9606"

/clone="148"
   and Kurosawa, Y
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Best Local Similarity 93.5%;
Matches 603; Conservative
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: n Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.

Location/Qualifiers
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BC022098
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Submitted (24-2AN-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                         662
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                                                                                                                                                                  TGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGC
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Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
inflo@bcggc.bc.ca
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/db xref="texxon:9606"
/clone="MGC:31944 MAGE:4878869"
/tissue type="Primary B-Cells from Tonsils"
/clone_lib="NHH MGC 48"
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/produc="Unknown (protein for MGC:31944)"
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/db_xref="GI:18380972"
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Mammalia; Eutheria;
1 (bases 1 to 919)
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/gene="IGL"
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/gene="IGL"
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/gene="IGL"
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/translation="MAWSPLLLTLIAHCTGSWAQSVITQPPSVSGAPCQRVTISCTGS
SSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAE
DEADYYCQSVDYSLSASGVFCGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSC
QVTHEGSTVEKTVAHFTCS"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                  919;
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                                                                                                                  Length
                                                                                                                                            Indels
                                                                                                             Score 566.4; DB 9;
Pred. No. 1.8e-136;
0; Mismatches 71;
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                                                                                                            79.7%;
illarity 89.2%;
Conservative
                                                                                                                           Similarity
                                                                    235
                                                                                                                                        Matches 635;
                                                                                                            Query Match
                                                                                                                           Local
                                                                   BASE COUNT
ORIGIN
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/translation="WKYLLPTAAAGLLLLAAQPAMAQSVLTQPPSVSAAPGQKVTISC
SQSSNIGSKYVSWYQQLPGTAPKLLIYDNNKRSPGSTPDRTPSGSKGSTAGTTGLQ
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Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Miura,K. and Kurosawa,Y.

Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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/protein_id="BAC01777.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="L9"
/clone="lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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                                                                                                                                                                                                                                                                           Direct Submission
Submitted (25-UUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutusukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
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ilarity 92.3%; Pred. No. 2.3e-136;
Conservative 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL:http://www.fujita-hu.ac.jp/immunity/
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                                        Query Match
Best Local Similarity 92.0%;
Matches 594; Conservative
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AUTHORS
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CQVTYEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGGGS"
                                                                                                                                                                                                                                                                                                                          AB064148 1GL mRNA for immunoglobulin lambda light chain VLJ Homo sapiens igr mRNA for immunoglobulin lambda light chain VLJ
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /produčt="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01776.1"
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="LB"

/clone lib="AIMS4"

/note="mixture of tissues:tonsils, umbilical cords,

peripheral blood and bone marrow"
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                                                                                                                                                                602 ACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGC
                                                GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGG
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukae-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L8
                                                                                                                                                                                                                       ATGAAGGGAGCACCGTGGAGACACAGTGGCCCCTACAGAATGTTC 707
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/gene="IGL"
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/gene="IGL"
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816 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:L7.
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Score 562.8; DB 9;
Pred. No. 1.6e-135;
0; Mismatches 52;
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62 AGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATCT 121
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256 c 232 g 164 t
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TGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
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          Direct Submission
Submitteed (25-JUN-2001) Yoshikazu Kurosawa, Institute for Submitteed (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@tujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site Please visit our web site URL:http://www.tujita-hu.ac.jp/immunity/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.2%; Score 562.8; DB 9; Length 816; 92.0%; Pred. No. 1.6e-135; .ive 0; Mismatches 52; Indels 0
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252 c 221 g 158 t
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
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548 CGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCAGT 607
                                                                                                                                         608 ATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGA 667
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fulita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mall:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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0; Mismatches 36; Indels
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                                                                                                                                                                                                              662 ATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTC
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Query Match 79.1%; Score 562.2; DB 9; Best Local Similarity 90.5%; Pred. No. 2.2e-135; Matches 600; Conservative 0; Mismatches 63;
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246 c 196 g 1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
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                                                                            128 CCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGC
                                                                                                          TCCCAGGAACGGCCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTT
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Ig lambda light chain;
Homo sapiens.
Homo sapiens
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YPGAVTVAWKADSSPVKAGVETTTFPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH
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hotes="J-segment"
383. .702
/gene="immunoglobulin lambda light chain"
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/gene="immunoglobulin lambda light chain"

    .51
    /gene="immunoglobulin lambda light chain"
52. .382

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/gene="immunoglobulin lambda light chain"
/note="variable region; V(lambda)I"
/gene="immunoglobulin lambda light chain"
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PGAVTVAWKADSSPKKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE
GSTVEKTVAPTECS"
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Human rearranged immunoglobulin lambda light chain mRNA.
X57806
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Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
2 (bases 335 to 381)
Combriato, G. and Klobeck, H.G.
V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
Eur J. Immunol. 21 (6), 1513-1522 (1991)
91257162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for overlapping sequences see: X51754-55, J00252-54; M15641-42.
Location/Qualifiers
1.747
/.rganism="Homo sapiens"
/isolate="individual ML"
  646
                                                  GCTGCCAGGTCACGCATGAAGGGACCGTGGAGAAGACAGTGGCCCCTACAGAATGTT 706
                          637
 ACGCGCCCAGCAGCTACCTGAGCCTGACGCTGAGCAGTGGAAGTCCCACAGAAGCTACA
              49. .379
/gene="immunoglobulin lambda light chain"
/note="variable region; V(lambda)I"
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/note="J-segment"
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tissue type="spleen"
'clone lib="phage library cML"
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Ig lambda light chain; immunoglobulin.
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Mammalia; Eutheria;
1 (bases 1 to 747)
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AB064141 821 bp mRNA linear PRI 02-JUL-2002 Home sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:Ll.
AB064141
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                              Length 747;
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/gene="immunoglobulin lambda light chain"
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244 c 196 g 138 t
                                                                                                                                                              78.8%; Score 560; DB 9; I
87.8%; Pred. No. 8.4e-135;
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                    Miura, K. and Kurosawa, Y. Construction of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
                                                                                                                                                                                                                                                                                                                                               1. .821

/croganism="Homo sapiens"

/db xref="taxon:9606"

/clone="L1"

/clone lib="AIMS4"

/note="maxture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
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                                                                                                                                                                     Direct Submission
Submitted (25-UNA-2001) Yoshikazu Kurosawa, Institute for
Submitted (25-UNA-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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260 c 228 g 158 t
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2 (bases 1 to 821)
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GTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGG
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BI837966 603083802
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AGENCOURT 8353624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279618
5', mRNA Sequence.
BQ711447, GI:21850346
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1 (Dases 1 to 952)

NIH-MGC http://mgc.nci.nih.gov/.

Nith-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution infermation can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2469 row: h column: 19
High quality sequence stop: 584.
I. 952
 BQ712280 A BQ710672 B BQ710674 B BQ710674 B BQ710672 B BQ756296 G B BQ756296 G B BQ756298 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756391 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ756128 G B BQ
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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COMMENT
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BQ711683 AGENCOURT
BG757730 GC2714835
BQ707953 AGENCOURT
BQ708246 AGENCOURT
                                                                                                           April 5, 2003, 19:13:54 ; Search time 1341.86 Seconds (without alignments) 8508.978 Million cell updates/sec
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1 ATGAGGGTCCCCGCTCAGGT......CCCCTACAGAATGTTCATGA 705
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               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                             nucleic search, using sw model
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UI-H-EZ1-602710483 603041960

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Score

Result

558.8 555.6 555.2 552 552 552

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/lab_host="bull MGC | phage-resistant)"
/lab_host="bull MG | phage-resistant)"
/lab_host="bull mgc | py oligo-dr priming. Directionally cloned into EcoR1; Cholm made by oligo-dr priming. Directionally cloned into EcoR1/Xhol sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Barkeley) using ZAP-chDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies). Note: this is a
                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 931)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                Contract: Robert Strausberg, Ph.D.

Contract: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM24'4 row: 1 column: 21

High quality sequence stop: 653.

High quality sequence stop: 653.

I. 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCCAGGTGCACGATGTGCCTATGAAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 TGACTCAGCCACCTCGGTGTCAGTGGCCCCAGGACGACGACATAACCTGTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 TGCTGGTCGTCAATGATGACAGCGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 ccaacterggaaacacgcccaccercarcarcacaggccaagccggggargaggccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 TACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT
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78.8%; Score 555.6; DB 14; Length 931;
Best Local Similarity 89.3%; Pred. No. 3.1e-133;
Matches 623; Conservative 0; Mismatches 69; Indels 6;
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                                                               /clone_lib=NIH_MGC_li3"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECGNI; cDNA made by oligo-dT prining. Directionally cloned
into EcoRI/AhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Geral M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
28. c 254 g 173 t 2 others
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       organism="Homo sapiens"
                             /db_xref="taxon:9606"
/clone="IMAGE:6279618"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov & column: 19
Plate: LLCM516 row: & column: 19
High quality sequence stop: 549.
                                                                                                                                                        574 CCACCACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGA 633
                                                                                                                                                                                                             CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAAGCA 667
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                            CCACCACACCCTCCAAACAAACAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGA
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SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 796)

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CONTACT: Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI703 row: f column: 10

High quality sequence stop: 795.

High quality sequence stop: 795.
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251 CCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTG
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226
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          /clone lib="NIH MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_hoft="Will MGC_48"
/lab_hoft="Will be phage-resistant"
/note="Organ: B-cells, Vector: pOTB7; Site 1: XhoI;
Site 2: BCORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACAGAGG(S. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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Matches 618; Conserv
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BQ707953 969 bp mRNA linear EST 16-JUL-2002 AGENCOURT\_8353606 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6279593

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/organism="Homo sapiens"
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/note=lorgan: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: Mote=lorgan: spleen; Vector: poTB7; Site_1: Xho1; Site_2: Google (colored liber) (colored liber) (colored liber) (colored liber) (colored liber) (colored liber) (colored liber) (diversity of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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5', mRNA sequence.
BQ707953
BQ707953.1 GI:21846852
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/db_xref="taxon:9606"
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I (bases I to 921)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone chrough the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov at: column: 22
High quality sequence stop: 628.
Location/Qualifiers
                                               CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCCGTCAAGGCGGGAGTGGAGA 547
428 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 487
               CGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAAGCA 667
                                                                                                                                                                    GCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCA 684
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Matches 604; Conservative
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AGENCOURT 8353529 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279636 5', mRNA sequence.
BQ712280
BQ712280.1 GI:21851179
EST.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 920)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail:inih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: column: 13
High quality sequence stop: 698.
63 GCCAGCATTACCTGGTGGGGAAACAACATTACAGGTAACAGTGTGCACTGGTACCAGGA 122
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                                                    171 GAAGCCAGCGCGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGAT
                                                                                                                                                       231 CCCTGAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGT
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BQ710672.1 GI:21849571
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/lab_host="DH10B" (phage-resistant)"
/lab_host="DH10B" (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                              DB 14; Length 920;
                                                                                                                                                                                                                                                                                                                            Score 548.8; DB 14; Length
Pred. No. 1.8e-131;
0; Mismatches 72; Indels
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         clone="IMAGE:6279636"
                                                                                                                                                                                                                                                                                                                                77.8%;
88.8%;
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.8
Matches 618; Conservative
                                                                                                                                                                                                                                                                216
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BQ710672
LOCUS '
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ORIGIN
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ACCESSION

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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG (3). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
Homo sapiens
Vakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 925)
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                                                                                        AIN-WGC http://mgc.nci.nth.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMS16 row: e column: 10
High quality sequence stop: 661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCT
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Pred. No. 4.6e-131;
0; Mismatches 73; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:6301041"
/clone=lib="NIH MGC 113"
/lab_host="DH10B" (phage-resistant)"
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_293 c 235
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Best Local Similarity 88.6%;
Matches 617; Conservative (
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200 357 440 417

300

597

657

320 537 260

477

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AGENCOURT 8616484 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302471 5', mRNA sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2519 row: p column: 24
High quality sequence stop: 687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 CTGAGCCTGACGCCTGAGCAGGAAGTCCCCACAGAAGCTACAGCTGCCAGGTCACGCAT 140
  439 GGCGGAGGGACCAAACTGACCGTCTTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTG 380
                                                                                                   619 CAGGCCCTGTGCTGGTCTATGATGATAGCGACCGGCCCTCAGGGATCCCTGAGGGA
                                                                                                                                                                                               559 TTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGTCGAAGCCGGG
                                                                                                                                                                                                                                                                 301 GATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGT----CTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 TTCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 GACTICIACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 GGAGTGGAGACCACACACCCTCCAAACAAAGCAACAACAAGAAGTACGCGGCCAGCAGCTAC
                                                                                                                                                                     241 TTCTCTGGCTCCAAATCAGGGAACACGCCACCCTGACCATCAACGGGGTCGAGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 GACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 CTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCAT
                                                                         181 CGGCCCCTATACTGGTCATCTATGATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGA
                                                                                                                                                                                                                                                                                             499 GATGAGGCCGACTATTACTGTCAGGTGTCCGATAGTGGTAGTGATCATCCTGTGCAATTC
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/clone="IMAGE:6302471"
/clone_lib="NIH_MGC_113"
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/lab_host="DH10B" (phage-resistant)"
/lab_host="DH10B" (phage-resistant)"
/note="Norgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECRI; Corgan: spleen; Vector: pOTB7; Site_1: Corgan: spleen; Vector: pOTB7; Site_1: Corgan: spleen; Vector: potentially cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAGGG(3). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a "212 c 253 g 185 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               602723726T1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4849878 3', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMIG50 row d column: 07
High quality sequence stop: 827.
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455 CCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACC 514
                                                                                                                                                                     575 CCACCACACCCCCCCAAAAGCAACAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGA 634
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                               S15 CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA
                                                488 CGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGA
                                                                                                                                         548 CCACCACACCTCCAAACAAAGAACAACAACAAGTACGCGGCCAGCAGCAACTACCTGAGCCTGA
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/clone="IMAGE:4849878"
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/clone="IMAGE:5217796"
/clone=lib="NIH MGC_118"
/tissue type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                  Contact: Robert Strausberg, Ph.D.
       (bases 1 to 754)
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Matches 622; Conserv
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/lab_hosts"DH10B (phage-resistant)"
/note="Vorgan: spiden; Vector: pOTBF; Site 1: XhoI; Site 2:
/note="Vorgan: spiden; Vector: pOTBF; Site 1: XhoI; Site 2:
/note="Vorgan: spiden; Vector: pOTBF; Site 1: Chord into EcoRI/XhoI sites using the following 5' adaptor:
/note EcoRI/XhoI sites using the following 5' adaptor:
/note ScoraCAGAG(3). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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603069019F1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5217796 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                       Query Match 77.4%; Score 545.8; DB 14; Length 908; Best Local Similarity 91.5%; Pred. No. 1e-130; Matches 590; Conservative 0; Mismatches 52; Indels 3;
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/note="vector: DCMV-SPORT6; Site_1: Not1; Site_2: EccRV (destroyed); RNA source leukcyctes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIM MGC Library."
                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.f column: 05
Plate: LLAM11547 row: f column: 05
High quality sequence stop: 749.
Location/Qualifiers
1. 754
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone="IMAGE:4853801"
/clone="IMAGE:4853801"
/clone="IMAGE:4853801"
/clone="IMAGE:4853801"
/clone="IMAGE:4853801"
/clone="IMAGE:4853801"
/clone="IMAGE:4853801"
/lab_host="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhOI;
Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for everage insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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602713568P1 NIH_MGC_48 Homo sapiens cDNa clone IMAGE:4853801 5',
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11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1700 row; g column: 18
High quality sequence stop: 786.
515 GGAGCCGTGACAGTGGCCTGGAAGAGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGAC 574
                                                                                                                                      635 GCCTGAGCAGTGGAAAGTCCCACAAAAGCTACAGGCTGCCAGGTCACGCATGAAGGGAGCA 694
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                                   549 CACCACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCTGAC
                                                           609 GCCTGAGCAGTGGAAGTCCCACAGAAGCTACA-GCTGCCAGGTCACGCATGAAGGGAGCA
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92.7%; Pred. No. 1.5e-130;
iive 0; Mismatches 43;
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AGENCOURT_6630576 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760519 BM924274
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NIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga.llnl.gov
Plate: LLAM12807 row: k column: 16
High quality sequence stop: 710.
Location/Qualifiers
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182 GGGCCCCTATACTGGTCATGATGATGATGACCGGCCCTCAGGGATCCCTGAGCGAT
                                                                                                                                431 TCTACCCGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCCGTCAAGGCGGGAG
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                                 134 AGGCCCCTGTGCTGGTCGTCTATGAAGATAGTGACCGGCCCTCAGGGATCCCTGAGCGAT
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/clone_lib="NIH MGC_116"
/lab_host="DH10B"
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pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon, 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is elstroyed upon cloning). Average insert size is 14 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                  Query Match 77.3%; Score 545; DB 14; Length 1086; Best Local Similarity 88.6%; Pred. No. 1.8e-130; Matches 614; Conservative 0; Mismatches 75; Indels 4.
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ACCESSION VERSION

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/organism="Homo sapiens"
/db xref="taxon:966"
/clone="INAGE:5301461"
/clone lib="NHH MGC l13"
/lab_host="DH10B (phage-resistant)"
/loce="Organ: spleen, Vector: pOTB7; Site_1: XhoI; Site_2: note: "Organ: spleen, Vector: poTB7; Site_1: XhoI; Site_2: ECBI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-CDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM2517 row: f column: 22
High quality sequence stop: 552.
High quality sequence stop: 552.
Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 917)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
/db_xere="Homo sapiens"
/clone="Ith="NIH MGC 113"
/clone="Ith="NIH MGC 113"
/clone="Ith="NIH MGC 113"
/lab host="Hol10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supprescript II RT (Life Technologies). Note: this is a
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AGENCOURT 8418138 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281593
SQT09509.1 GI:21848408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2474 row: k column: 02
High quality sequence stop: 635.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 949)

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                                           CCACACCCCTCAAACAAAGGAACAACAAGTACGGGGCCAGGAGGTACCTGAGCCTGAGCC
                                                                                                                                                                                                                                                                          CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCC 694
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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251 CCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTG 310
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131 GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGGGGCCCCTA 190
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                                                                                                                                               203 TCCTGGTCGTCTCTGCTGATACCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCCT
                                                                                                                                                                                                                                                                                                                                     311 ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCC---GGTCTTCGGAGGAGGA
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Macaque prinatized
DNA sequence of a
Ant-CD4 monkey-hum
Human bladder tumo
DNA encoding novel
Macaque prinatized
DNA sequence of a
Primatised anti-hu
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8205.894 Million cell updates/sec
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## ALIGNMENTS

Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA. Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss. Brams P, Hanna N, Shestowsky WS; AAT62509 standard; DNA; 705 BP 96WO-US10053 95US-0487550 Chimeric Macaca cynomolgus; Chimeric Homo sapiens. 25-MAY-1997 (first entry) (IDEC-) IDEC PHARM CORP. Anderson DR, WO9640878-A1 06-JUN-1996; 07-JUN-1995; 19-DEC-1996, RESULT 1  (first entry)

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                                                                                                      primatised forms (AAW01817 and AAW01818) of the light and heavy chained cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes are inserted into heavy chain constant region genes to allow prodn. of priman light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 78 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                 Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
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time sequence encourse a primarized toum of the adultony viril tight contains acquaine encourse a primarized toum of the sequence. This sequence is used in a method which studies now monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28 Such Mab's are specific immunosuppressants for treatment of Giseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus srythematosus, type I diabetes mallitus, rheumatorid arthritis, peoriasis, aplastic ansemia, inflammatory bowel disease, allery and multiple sclerosis, graft vs. host disease, allery and multiple sclerosis, graft vs. host disease, no inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleuvin-2.7.7.
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                                                                 Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-diotype reagent; interleukin-2; IgG; immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a primatized form of the antibody 7C10 light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;
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. 4e-167;
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antigen-specific immunoglobulin G (IgG) responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= 7C10 light chain
Macaque primatized 7C10 light chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brams P, Hanna N;
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                                                                                                                                                                                                                                            cell proliferation; ss.
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Matches 705; Conserv
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1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCCAGGTGCACGATGT

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WO200189567-A1.

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Human, macaque monkey; light chain; primatised antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7 1 antigen; CD80; B7 2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-ve-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
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                                       1 ATGAGGGTCCCCGCTCAGCTCCTGGGCCTCCTGCTCTCGGCTCCCAGGTGCACGATGT 60
                                                                                                    GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATC
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/*tag= a
/product= "Light chain of 7C10 antibody"
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Chimeric - Macaca sp.
Synthetic.
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD86) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for inducing the apoptosis of B7+ cells. The invention is useful for inducing the apoptosis of B7+ cells. The invention is a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopania purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-hoot disease. The antibody is useful for immunosuppression or graft-vs-hoot disease. The antibody is useful for immunosuppression or graft-vs-hoot disease. The antibody is useful for immunosuppression crimen or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive and hyperproliferative collicis, food-related allergies e.g. migraine, thinitis and eczema, and other types of allergies. The present nucleic caid sequence encodes the light chain of 7010, a primatised antibody used in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2).
                                                                                                                                                                                                                                                                                                                                                                        Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Fig 3a; 89pp; English.
                                                                                                                                                                                                                                                          Anderson DR, Hanna N, Brams P;
                                                                                                                                                             22-MAY-2000; 2000US-0576424.
                                                                                                                22-MAY-2001; 2001WO-US16364
                                                                                                                                                                                                          (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                       WPI; 2002-089895/12.
                                                                                                                                                                                                                                                                                                                             P-PSDB; AAU11538.
                                                                   29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A DNA sequence (AAT62867) codes for lambda variable and constant domains (AAW14924) of anti-human CD4 monkey/human chimeric antibody CE9.1. This antibody contains the antigen binding domains (see also AAW14922-23) of a cynomolgus monkey anti-CD4 monoclonal antibody, a human heavy chain constant region of gamma 1 isotype and GM1a, GM1z allotype, and a human lambda light constant region of the Oz minus, mcg minus genotype and Re minus allotype. The immunoglobulin genes were cloned into mammalian expression vector
GGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTGTTC
                               361 GGAGGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC
                                                              CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC
                                                                                           cceccercercasasascencasasceasasceasasceasasceasascencarasasceas
                                                                                                                            TTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGA
                                                                                                                                               GTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTG
                                                                                                                                                                                                                           GTGGAGACCACCACACCCTCCAAACAAAGAACAACAAGTACGCGGCCAGCAGCTACCTG
                                                                                                                                                                                                                                                          AGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, esp. useful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                           661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
                                                                                                                                                                                                                                                                                                                        GGGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCATGA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ant-CD4 monkey-human chimeric antibody CE9.1 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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Chimaeric Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT62867 standard; DNA; 702
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                                                                                                                                                                                                                                                                                                64 TATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACC 123
                                                                                                                                                                                                                             63
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                                                                                                                                                                                              Gaps
TCAE 6, and chimeric antibody was produced in CHO cells. CE9.1 binds to domain 1 of human, but not macaque, CD4, a region involved in the interaction with MHC class II molecules on antigenpresenting cells. It shows potent immunomodulatory activity with low immunogenicity in humans, and can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
                                                                                                                                                                                                                             4 AGGGTCCCCGCTCAGCTCCTGGGCCTCCTGCTCTGGCTCCCAGGTGCACGATGTGCC
                                                                                                                                                                                                                                                  1 ATGGCCTGGGCTCTGCTCCTCGTTGCTCACTTACAGACTCTGCGGGCCTCC
                                                                                                                                                                                                                                                                                                                      244 TCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGT
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                                                                                                                                                                                                                                                                                                                                                                   124 TGTGGGGGAGACAACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544 GAGACCACCACACTCCAAACAAAGCAACAACAAGTACGGGGCGAGCTACCTGAGC
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0
                                                                                                                                                       Score 585.2; DB 18; Length 702; Pred. No. 4.1e-137; O; Mismatches 73; Indels O;
                                                                                                                        Sequence 702 BP; 151 A; 217 C; 207 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705
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                                                                                                                                                       83.0%;
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                                                                                                                                                                                          Matches 629; Conservative
                                                                                                                                                           Query Match
Best Local Similarity
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
404 AGCTGACCGTCCTAGGTCAGGCCGAAGGCTGCCCCTCGGTCACTCTGTTCCCGCCCTCCT 463
                                                                                                                                                                CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAACACCG 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGCAGTGGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCG 703
                                                                                                                   CTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCGGG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      CCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                584 CCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGC
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                                                                                                                                                                                                                                                                  GAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #19286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671 TGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                704 recasasacacidececeracacaarerear 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS83482 standard; cDNA; 836 BP
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel polypeptide fragments (I) and the polynucleotides (II) that encode them that are highly expressed in a human bladder tumour and which have expostatic activity. (II) are used to recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for treatment of bladder cancer, to directly treat this form of cancer (including expression from gene directly treat this form of cancer (including expression from gene is also used for the generation of specific antibodies. (II) are identified by assembling ESTS (expressed sequence teags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAZ43260-243309 represent expressed sequence tag (EST) fragments isolated from a human bladder tumour cDNA library which encode the proteins represented in AAY66143-Y66198.
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Pred. No. 2e-136;
0; Mismatches 59; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (META-) METAGEN GES GENOMFORSCHUNG MBH.
treatment; gene therapy; EST; ss.
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Best Local Similarity 91.1%;
Matches 631; Conservative (
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                 The polypeptide and polynuclebride sequences have applications in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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  disorders involving aberrant protein expression or biological activity.
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                                                                                                                                                                                                                                                                                           Ouery Match 78.8%; Score 555.6; DB 23; Length 836; Best Local Similarity 91.6%; Pred. No. 1.1e-129; Matches 588; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                     Sequence 836 BP; 185 A; 262 C; 232 G; 157 T; 0 other;
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This sequence encodes a primatized form of the antibody 16C10 light chain from macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to monoclonal antibodies binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autofimmune diseases, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, nost diseases, B cell lymphoma, inflections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be confugated to a drug or toxin. MAD's or their fragments, can also be used as imaging agents and as vaccines or immunosupersessutes allockines mill molecule immunosuppressants. Blockines B/Ockines interactions or induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppresses.
CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
              T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACCTGTGGGGG-----AGACAACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCGCGCCCCTATACTGGTCATCTATGATGGTGACCGGCCCTCAGGGATCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;
                                                                                                                                                                                       /*tag= a
/product=16C10 light chain
                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Fig 5a; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson DR, Brams P, Hanna N;
                                                                                                                                                                                                                                                                                                                                              97WO-US19906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-286601/25.
                                                                                                       Macaca fascicularis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, macaque monkey, light chain, primatised antibody, 16C10 antibody, neuroprotective, apoptosis inducer; allergy; CD28 receptor antagonist, 87_1 antigen; CD80, B7_2 antigen; CD86, B Cell cancer; mecastasis, tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence of a primatised form of the light chain of 16C10 antibody.
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CCAGGAACGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT 240
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                                                           GCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTC 354
                                                                                                                                       CTGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 474
                                GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG
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                                                                                                                                                                                                                                                          TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
                                                                                                                                                                                                                                                                      661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
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/product= "Light chain of 16C10 antibody"
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                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Homo sapiens
- Macaca sp.
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of .B7 the invention is concer inducing the apoptosis of .B7 the invention is a cancer where B calls promote the growth and/or metastasis of tumours, B call lymphoma, B call lawrends, and autoimmune diseases such as a concer where B calls promote the growth and/or metastasis of tumours, B call lymphoma, B call lawrends, and autoimmune diseases Buch as diopathic thrombocytopenia purpura, systemic lupus, erythematcosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative collitis, food-related allergies e.g. Crohn's caimays disease, and other types of allergies. The present nucleic acid sequence encodes the light chain of 16c10, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                            Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCCAGGACAGACGGCCAGGATC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;
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Matches 612; Conservative
2002-089895/12.
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GCCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCCAGGACAGACGGCCAGGATC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 DNA sequences (AAT62512 and AAT62513) respectively code for primatised forms (AAM01821 and AAW01822) of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                              Primatised anti-human B7.1 antigen antibody 16C10 light chain DNA
                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18; Length 711;
                                                                                                    CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705
                                                                                                                     CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.4%; Score 538.6; DB 18; Length
85.9%; Pred. No. 2e-125;
iive 0; Mismatches 94; Indels
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                                                                                                                                                                                                        AAT62512 standard; DNA; 711
                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
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P-PSDB; AAW01821.
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Best Local Si
Matches 611
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Human, ovarian antigen; ovary; ovarian; breast, cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst, dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gentcontestinal disorder; urinary system disorder; drug screening; gent cherapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ACCTGTGGGGG-----AGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAG
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                                                                                                                                                                                     GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAG
                                                                                                                                                                                                                          241 gaccgarrcrcrcgcrccaagrcrggraccgcgccrcccrggccarcarggcrccag
                                                                                                                                                                                                                                                               GCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTC
                                                                                                                                                                                                                                                                                                                                    TTCGGAGGAGCCCCGGGTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCGGTCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 GCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
                                                                                                                CCAGCGCGCGCCCTATACTGGTCATCTATGATAGTGACCGGCCCTCAGGGATCCCT
                                                                                                                                                181 ccassaacesccccaacrccrcarcrareacarraacaaccacccrcassaarrrcr
                                                                                                                                                                                                                                                                                                                                                                                                              CTGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAAGGCCACACAGGTGTGTCTCATA
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Local Similarity

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                                                                                                                                                                                                                                                                                                                            The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABP4131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumnours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polyardome, ovarian oranges, and dysmenorinosa), endocrine disorders, infections (e.g., chiammydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and vaginitis), immune disorders (e.g., congenital and acquired insorders, nucleotides (e.g., anaemia), cardiovascular disorders, oblood-related disorders (e.g., anaemia), cardiovascular disorders, nucleotides may also be used in screening for compounds which indulate ovarian antigen expression or activity. The polymcleotides may further be used for gene therapy, chromosome mapping, in the modulate ovarian antigen expression or activity. The polymcleotides may be used as food additives or to prepare antibodies useful in disease diagnosis, drum an ovarian antigen of the invention of individuals and in forensic analysis, and the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGTGGGGGGGGAGACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 AGTCCCTGTGCTGTCATCTATCAAGATAACAASCGGCCCTCAGGGATCCCTGAGCGAT 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                    Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCCCCTATACTGGTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 318; 2922pp; English.
                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                    07-JUN-2000; 2000US-209467P.
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  07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 576; Conservative
                                                                                                                                                                                                                                                                  neurological diseases -
                                                                                                                Rosen CA;
                                                                                                                                                  2002-147878/19.
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P-PSDB; ABP41361.
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ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361

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The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (I) is useful a hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
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432 ATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCARCACTG------KGGTATTCGGCG 485
                                      421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                            TCTACCGGGGGGCGTGACAGTGGCCTGGAAGCCAGATAGCAGCCCCGTCAAGGCGGGAG
                                                                                                                                           CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACACGGGTGTGTTCTCATAAGTGACT
                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                      GAGGGACCCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCC
                                                                                                                   CGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACAGGTGTGTCTCATAAGTGACT
                                                                                                                                                                                                TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGGG
                                                                                                                                                                                                                                                                               TGGAGACCACCACCCTCCAAACAAGCAACAACAAGTACGCGGGCCAGCAGCTGA
                                                                      GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCCCGGTCACTCTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   786 GGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 827
                                                                                                                                                                                                                                                                                                                                                                                                                                         662 GGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #19290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS83486 standard; cDNA; 841 BP.
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23-AUG-2000; 2000US-0649167.
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Human cDNA encoding secreted potein SECP38.
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P-PSDB; AAU82012.
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensiss, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
                                                                                                                                                                                                                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         262 TCTCTGGCTCCCAACTCTGGGAACACAGCCACTCTGACCATCAGGGGACCCAGGCTATGG
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                                                                                                                                                                                                             74.3%; Score 524; DB 23; Length 841;
89.7%; Pred. No. 9.3e-122;
tive 0; Mismatches 60; Indels 6
                                                                                                                                                                                       Sequence 841 BP; 191 A; 273 C; 224 G; 153 T; 0 other;
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The invention relates to forty four human secreted proteins (referred to as SECP-1 to SECP-44) and the nucleic acids encoding them. Also included are a host cell transformed with the nucleic acid, a cranspenic animal comprising the nucleic acid, an anti-SECP actions of the SECP proteins in isolating agonists and antagonists of SECP activity and a method of isolating compounds which alter the expression of the SECP nucleic acid. The SECP polynucleotides and polypeptides are useful in the diagnosis, treatment and prevention of cardiovascular (e.g. atherosclerosis, hypertension, myocardial in the diagnosis, treatment and prevention of cardiovascular (e.g. atherosclerosis, hypertension, myocardial in the diagnosis, treatment and prevention of cardiovascular (e.g. atherosclerosis, bypertension, myocardial in the cardiovascular (e.g. buchenne and Becker muscular (e.g. cancer), developmental (e.g. buchenne and Becker muscular disprachy, and neurological (e.g. epilepsy, Alzheimer's disease) disorders. Numerous other examples of each disorder are given in the specification. The present sequence is a CDNA encoding a SECP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forty four human secreted proteins (referred to as SECP-1 to SECP-44), useful in the diagnosis, treatment and prevention of cardiovascular (e.g. atherosclerosis), autorimmune/inflammatory (e.g. allergies) and cell proliferative disorders
                                         immunosuppressive; antiviral; anti-HIV; antiarthritic; antirheumatic; muscular active general; anticonvulsant; noctropic; neuroprofecctive; antialergic; hypotensive; cardiovascular disorder; atherosclerosis; hypotensive; cardiovascular disorder; atherosclerosis; inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy; rheumatoid arthritis; cell proliferative disorder; cancer; developmental disorder; buchenne muscular dystroph; neurological disorder; epilepsy; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue H, Elliott VS, Tribouley CM, Lee EA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu DAM;
gene; SECP; antiinflammatory; cytostatic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman JL, Tang YT, Yue H, Elliott VS, Tribouley Rankumar J, Lal P, Xu Y, Warren BA, Hafalia AJA, Azimzai Y, Batra S, Burford N, Yao MG, Nguyen DB, Walia NK, Gandhi AR, Au-Young J, Patterson C;
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27-JUN-2000; 2000US-21460IP.
31-JUL-2000; 2000US-222372P.
08-SEE-2000; 2000US-231435P.
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09-APR-2002 (first entry)

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Human; novel protein; 88; Antianaemic; osteopathic; antinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritts; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                               543
                                                                            GAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA 363
                                                                                                                                                                                                GGGACCCGGGTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG 423
                                                                                                                                                                                                                                                          CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC 483
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124 TGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGGGG 183
                                                                                                                  TCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
                                                                                                                                               294 tridecrickágorckágákonáragóckáchrigacráragragágockagáragagágir 353
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                           174 recrerégágárgearreccáááanáárárécrrárrégraccaécagaagreageceag 233
                                                                                                                                                                                                                                                                                                                                                              TACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding a novel human protein #283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue regeneration; immune disorder.
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AAS22717 standard; cDNA; 869
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The invention relates to polynuclectides encoding novel human proteins or their active domains. The polypeptides in a method of artibodies raised against the polypeptides are used in a method of reatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as conclusive weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to raise antibodies/elicit an immune response, to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Content and/or nerve tissue, wound healing, treating blacelet disorders, stem cell disorders, regenerating bone, carrilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis anemain, and elecates, at the cell disorders, regenerating one contraceptive, treating osteoporosis and osteoarthritis, anemain, inferior may also be used.
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                                                                                            Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sclerosis, stroke, immune deficiencies resulting from Dacterial, vir. fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCCTCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 869 BP; 164 A; 219 C; 272 G; 214 T; 0 other;
                                                                                                                                                               Claim 1; Page 695; 894pp; English.
                         WPI; 2001-451939/48.
P-PSDB; AAU14412.
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us-09-758-173-1.rng

Sequence 791 BP; 183 A; 252 C; 208 G; 148 T; 0 other;

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polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as inaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences Assayled represent novel human or amino acid sequences. Assayled represent movel human Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from Wipo at fip. wipo.int/pub/published_pot_sequences.
                      661
                                                                                                      252 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGGTGCCAGGTCACGCATGAAG 193
542 TGGAGACCACCACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                           GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                                      662 GGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCAT 703
                                                                                                                                                                         192 GGAGCACCGTGGAGAAGACAGTGCCCCTACAGAATGTTCAT 151
                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #23075.
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG23084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247
                                                                                                                                      62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCCAGGACAGACGGCCAGGATCA 121
                                                                                                                                                                                    CCTGTGGGGGGAGACAACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC 181
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                                                                                                                                                                                                                                                                                                                                                                                                     GGGCCCCTATACTGGTCATCTATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGAT
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       Score 516; DB 23;
Pred. No. 9.2e-120;
0; Mismatches 65;
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       73.2%;
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                                                                   Matches 571; Conservative
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02-AUG-2001.

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The invention relates to polymuclectides encoding novel human proteins or their active domains. The polypeptides in a method of antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as montal polypeptides are used to identify compounds which bind to the polypeptides. Polymucleotides of the invention are used as probes and principles, Polypeptides of the invention are used as probes and production of recombinant proteins, and in generating anti-sense DNA or trarget drugs to a tumour, in assays to determine biological activity, to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine duantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, alsorders, stem cell disorders, wound healing, treating purns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia contraceptive, treating osteoporosis and osteoarthritis, anaemia sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, and infection.
                                                                                                                                                                                                                                                                                          Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage
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                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 721-722; 894pp; English.
                                                                                                                                                                               Tang YT, Liu C, Drmanac RT
                                           25-JAN-2001; 2001WO-US02623.
                                                                                     25-JAN-2000; 2000US-0491404
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                                                                                                                                   (HYSE-) HYSEQ INC.
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465 GTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAG 524
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Title: Perfect score: Sequence:	US-09-758-173-1 705 1 ATGAGGTCCCCGCTCAGCTCCCCTACAGAATGTTCATGA 705	
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Searched:	2054640 segs, 14551402878 residues	
Total number of	Total number of hits satisfying chosen parameters: 4109280	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	R108862	AR135374 Sequence AB064177 Homo Bapi	BC028090 Homo sapi	X57812 Human rearr X57821 Human rearr	AJ309319 Homo sapi	AR108866 Sequence AR064230 Homo gani	AB064174 Homo sapi	AB064176 Homo sapi	BC022823 Homo sapi	X57802 Human rearr	AB064168 Homo sapi	AX402510 Sequence	AB064179 Homo sapi	X57818 Human rearr	AB064184 Homo sapi	E01593 cDNA encodi M18645 Human Iq re	AX232564 Sequence	AB064210 Homo sapi AB064209 Homo sapi	X57813 Human rearr	AB064213 Homo sapi AB064185 Homo sapi	AB064214 Homo sapi	AB064165 Homo sapi xc7810 Himan rearr	X57805 Human rearr	AB064173 Homo gapi	ABO64111 HOMO BADI	AB064233 Homo sapi	AB064183 Homo sapi		~	AB064180 Homo sapi AB064212 Homo sapi	-			linear PAT 14-FEB-2001				ω.	s and transfectomas	
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% Query Match Length 1	705	83.0 702	1.0	8.6	7.0	9.6		5.1	. 1.	د. م د. د	. 4.	9.0		2.5	9.0	9 9.	2.5	4. 4.	2.5	2.0	1.9	6.6	1.5	٠. ١٠٠	. 9.	4.0	m c	7.	0.0	w 0				862 nce 1 from patent 862	.1 GI:12	wn.	Unclassified.	ases 1 to 705) son, D.R., Brams, P	i g	S
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                  Query Match 83.0%; Score 585.2; DB 6; Length Best Local Similarity 89.6%; Pred. No. 6.6e-133; Matches 629; Conservative 0; Mismatches 73; Indels
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AUTHORS
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100.0%; Score 705; DB 6; Length 70
Best Local Similarity 100.0%; Pred. No. 3e-162;
Matches 705; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 702)
Hanna,N., Newman,R.Anthony. and Reff,M.Elliot.
Recombinant anti-CD4 antibodies for human therapy
Patent: US 6136310-A 5 24-OCT-2000;
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Sequence 5 from patent US 6136310.
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DBADYYCWDSSSDHVVPGGGTKITVLGQPKAAPSYTLEPPSSBELQANKATLVCLI
SDFYPGAYTVANKADSSPVKACVFTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQ
VTHECSTVEKTVAPKFCSARQSTPFVCEXQGQSSDLPQPPVVAGGGSGGGSGGSG
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               Miura, K. and Kurosawa, Y. Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="immunoglobulin lambda light chain VLJ region"
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Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="AlMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
                                                                                                                                               Direct Submission
Submitted (25-UNN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-dho, Toyoake 470-1192, Japan (E-mail:kurosawaébujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site UKL:http://www.fujita-hu.ac.jp/immunity/.
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/db_xxef="taxon:9606"
/clone="L37"
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'db_xref="GI:21669561"
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Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Bakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,O.L.,
Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
VogerJoll., Walker,M.A., Wetherby,K.D., Touchman,J.W., Tsurgeon,C.,
Zhang,L.-H. and Green,E.D.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: RAK Plate: 62 Row: k Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC028090 901 bp mRNA linear PRI 01-MAY-2 Homo sapiens, clone MGC:40381 IMAGE:4184029, mRNA, complete cds.
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                                                                                                                                                                                548 TGGAGACCACCACCCTCCAAACAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGA 607
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                                                                                                                                                                                                                                                                    602 GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAG 661
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Tissue Procurement: David N. Louis, M.D.
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
488 TCTACCCGGGGGCCGTGACAGTGGCTTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGAG
                                                                                                     542 TGGAGACCACCACCCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGCTACCTGA
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Contact: MGC help desk
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/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="MGC:40381 IMAGE:4184029"

/clone="MGC:40381 iMAGE:4184029"
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Best Local Similarity
Matches 596; Conserv
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ORIGIN
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AUTHORS
TITLE
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MEDLINE
PUBMED
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                                 REFERENCE
AUTHORS
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DYYCQLWDSSSDHPVVFGGGTKLTVLGQPKAAPSVTLFPPPSSEELQANKATLVCLISD
FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEGWKSHRSYSCQVT
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Human rearranged immunoglobulin lambda light chain mRNA.
K57812
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Pred. No. 1.8e-129;
0; Mismatches 58; Indels 6
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Best Local Similarity 90.8%;
Matches 632; Conservative
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X57812.1 GI:33723 Ig lambda light chain; immunoglobulin.

Homo sapiens. Homo sapiens

KEYWORDS SOURCE ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 803)

Klobeck, H.G.

Direct Submission

NL Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany

E (bases 34) to 393)

Combriato, G. and Klobeck, H.G.

Vlambda and Jlambda-Clambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism

Eur. J. Immunol. 21 (6), 1513-1522 (1991)
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XPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEGWKSHRSYSCQVTH
EGSTVEKTVAPTECS"
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354. .391
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/note="'d-segment"
392. .711
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/note="constant region"
254 c 226 g 146 t
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/clone_lib="phage library cML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/isolate="individual ML"
/db_xref="taxon:9606"
/chromosome="22"
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PGAVTvawkadsspvkagvetttpskQsnnkyaassylsltpeQwkshrsyscQvthe
GSTVEKTVAPTECS"
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/gene="immunoglobulin lambda light chain"
/note="variable region; V(lambda)III"
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/gene="immunoglobulin lambda light chain"
/note="J-segment"
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/gene="immunoglobulin lambda light chain"
                                                                                                                                                                                                                                                                                                385. .704
/gene="immunoglobulin lambda light chain"
                                                    /gene="immunoglobulin lambda light chain"
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Pred. No. 3.6e-127;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                             135
                                                                                 /proteIn_id="CAA40958.1"
/db_xref="GI:33742"
                                                                                                                                                                                                                                                                                                                              /note="constant region'
230 c 211 g 1
                            'evidence=experimental
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Best Local Similarity 93.1%;
Matches 598; Conservative (
             'note="cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet 2 (bases 340 to 386) (Muenchen, Shillarstr. 44, 8000 Muenchen 2, Germany (Combriator, G. and Klobeck, H.G. V lambda and J lambda C lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and Eurarrange by a deletion mechanism

Eur. Immunol. 21 (6), 1513-1522 (1991)
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1 (bases 1 to 747)
Klobeck, H.G.
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                                                                                                                                                                                                                                                                                                                                                                for overlapping sequences see: X51754-55; J00252-54; M15641-42.
Location/Qualifiers
1. .747
242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGGG
                   ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGGTAGTGATCATCCGGTCTTCGGAG
                                                                         CGCCCTCCTCTGAGGAGCTTCAAGCCAAACAAGGCCACACTGGTGTGTCTCATAAGTGACT
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/gene="immunoglobulin lambda light chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="spleen"
/clone_lib="phage library cML"
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X57821.1 GI:33741
Ig lambda light chain; immunoglobulin.
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/asolate="individual ML"
/db_xref="taxon:9606"
/chromosome="22"
/clone="cML70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell_type="B-cell"
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Homo sapiens
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HSIGVL031
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Location/Qualifiers
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Best Local Similarity 86.11
Matches 612; Conservative
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LILLYVDGDRBSGIPDRESGNSESARATLISWAPAPABADEAPPTCQWAPTGG
LILLYVGQPKAAPSYTLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA
GVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS"
                                      HSA309319 648 bp mRNA linear PRI 16-NOV-2001
Homo sapiens partial mRNA for anti-peptide/NHC complex
HLA-A1/MAGE-A1 monoclonal antibody light chain.
                                                                                                                                                                                                                                                                                                                                                     Chames, P.
Direct Submission
Submitted (14-MAY-2001) Chames P., Pathology, Azm, P. Debyelaan 25, 6202AZ Masstricht, NETHERLANDS
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                                                                                                       AJ309319.1 GI:16974103
constant region; immunoglobulin light chain; monoclonal antibody;
variable region.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/product="immunoglobulin light chain constant region"
| 199 c 182 g 115 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 TCTGGCTCCAATTCTGAGAGCGCGGCCACCCTGACCATCAGTATGGTCGCCGCACCCGCAGAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 TATGAACTGACTCAGCCACCTTCGGTGTCAGTGTCCCCAGGACAGACGCCAGGATCACC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304.GAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAGGA 363
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328. .>648
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                                                                                                                                                                                                                                                              TCR-like Himan anti MHC-peptide antibodies: peptide fine-specificity is possible over a wide range of affinity Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="anti-peptide/MHC complex HLA-A1/MAGE-A1
monoclonal antibody light chain"
/protein id="CAC85285.1"
/db_xref="GI:16974104"
                                                                                                                                                                                                                                              Chames, P., Rojas, G., Dieckmann, D., Rem, L., Schuler, G. and
Hoogenboom, H.R.
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/function="immune response"</pre>
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/db_xref="taxon:9606"
/rearranged
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   RESULT 7
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                                                                                          ACCESSION
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1 (bases 1 to 711)
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C. Human B7.1-specific primatized antibodies and transfectomas expressing said antibodies
Patent: US 6113898-A 9 05-SEP-2000;
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                                                         307 GGGACCAAGCTGACCGTCCTCGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCA 366
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                                                                                                                                                                           367 CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC 426
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                                                                                                                     424 CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                   487 GAGACCACCACCACCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGCTACCTGAGC
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Sequence 9 from patent US 6113898.
AR108866
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DEADYYCOVMDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD
FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPPEQWKSHRSYSCQVT
HEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                         196 GTGCTGGTCATCTATAGGGATAGCAACCGGCCCTCTGGGATCCCTGAGCGATTCTCTGGC 255
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                                                                                                                                                                                                                                              CTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGTGGG 129
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Homo sapiens
                                                                                                                                                                          Length 790;
                                                                                                                                                                                                           Indels
                                                                                                                                                                      Score 538; DB 9; I
Pred. No. 2.4e-121;
0; Mismatches 45;
                                                      1. .66
/gene="IGL"
/note="pelB signal peptide"
238 c 223 g 146 t
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ilarity 91.9%;
Conservative (
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                                                        sig_peptide
                                                                                                                                                                                                         Matches 581;
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/codon start=1
/producft="immunoglobulin lambda light chain VLJ region"
/producft="immunoglobulin lambda light chain VLJ region"
/protein id="BACO1865.1"
/db_xreff="G1:21669667"
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/translation="MKXLLPTAAAGLLLLAAQPAWANFMLTQPLSVSVALGQTARITC
GGNNIGSKNVHWYQQKPGQAPVLVIYRDSNRPSGIPERFSGSNSGNTATLTISRAQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 02-JUL-2002
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Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB064230 790 bp mRNA linear PRI 02-JUL-
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:L90.
AB064230
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                                                                                                                                                                                                                                                            GCGGGAGTGGAGACCACCACCCTCCAAACAAAGAACAACAAGTACGCGGCCAGCAGCAGC
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L. Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan (E-mall:kurosawa@fujite-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_cref="L90"
/clone="L90"
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
                                                                                                                                                                                  GCGGGAGTGGAGACCACCACCACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
                                                                                                                                                                                                                                                                                                                                        AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG
             Treggaggaggagecegggtgacegreerageceaaggergececreggreacr
                                                                                    CTGTTCCCGCCCTCCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTCTCTCATA
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L90
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Unpublished
2 (bases 1 to 790)
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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AUTHORS
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JOURNAL
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AB064230
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Kurosawa, Y.
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                 Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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                                                                                                                Direct Submission

Direct Submission

Submitted (15-JUM-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;

Kutsukake-cho, Toyoake 470-1192, Japan

Kutsukake-cho, Toyoake 470-1192, Japan

Femail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site

URL:http://www.fujita-hu.ac.jp/immunity/.
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peripheral blood and bone marrow"
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Pred. No. 1.8e-120;
0; Mismatches 66;
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244 c 246 g 164 t
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VTHEGSTVEKTVAPTECSARQSTPFVCEXQGQSSDLPQPPVNAGGGSGGGSGGGEG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;
Kutsukke-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.tujita-hu.ac.jp/immunity/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:L36.
Homo sapiens
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                  Comprehensive Medical Science, Fujita Health University;
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                                      Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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Pred. No. 1.7e-118;
0; Mismatches 71;
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/organism="Homo sapiens"
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/clone="L27"
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Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
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     Score 529.6; DB 9; Length 824;
Pred. No. 2.7e-119;
0; Mismatches 69; Indels 0
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AUTHORS
TITLE
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REFERENCE AUTHORS

TITLE JOURNAL

REMARK COMMENT

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Michaeck, H.G.
Direct Submission
Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische Chemie, Physikalische Biochemie und Zellbiologie der Universitaet Greme, Shillerstr. 44, 8000 Muenchen 2, Germany 2 (bases 355 to 401)
Combriato, G. and Klobeck, H.G.
Combriato, G. and Klobeck, H.G.
W. lambda and J lambda-[lambda gene segments of the human immunoglobulin lambda light chain locus are separated by 14 kb and rearrange by a deletion mechanism
Eur. J. Immunol. 21 (6), 1513-1522 (1991)
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Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bumannalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 725)
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ALPKQYAYWYQQKPGQARVLVIYKDNERPSGIPERFSGSSSGTTVTLTISGVQAEDEA
DYYCQSADSSGTYWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOU22823 895 bp mRNA linear PRI 07-FEB-2002 Homo saplens, clone MGC:39283 IMAGE:4856249, mRNA, complete cds. BC022823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 42 Row: g Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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/clone lib="NIH MGC 48"
/lab host="DH10B-R"
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/protein_id="AAH22823.1"
/db_xref="GI:18606084"
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Contact: MGC help desk
                                                                                                                                                                                                  701
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="MGC:39283 IMAGE:4856249"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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BASE COUNT ORIGIN

CDS

FEATURES

541 575

515

635 661 695

601

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890 bp mRNA linear PRI 26-JUN-2002
Homo sapiens, clone MGC:40425 IMAGE:5177123, mRNA, complete cds.
BC032452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Web site: http://www.nisc.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Boulfard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Magtrian,S.D. McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLML at: http://image.llnl.gov estries: IRAK Plate: 64 Row: f Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Bureleostomi;
Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
1 (bases 1 to 890)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-UN-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="Brain, Lung, Testis, adult, pooled whole" /clone Lib="NIH MGC 115" /lab host="DH10B"
                                                                      496 TCTACCCGGGGGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG 555
                                                                                                                                                                              556 TGGAGACCACCACACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGA 615
                                                                                                                                                                                                                                                  GCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAG 661
                                                                                                                                                                                                                                                                                482 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCCGTCAAGGCGGGAG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                542 TGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGA
                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="MGC:40425 IMAGE:5177123"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC032452.1 GI:21595391
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BC032452
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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COMMENT
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TLGDKCAWQQKPGPSPLVIPODSKRASGTPERFEGSSNSGNTATLIGSTQANDEA
DYVCQKANGSTAFFYDGGGTKLTVLGQPK&ABSYELFPPSSEELQANKATLVCLISDFYP
GAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLELPPEQWKSHRSYSCQVTHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                      for overlapping sequences see: XS1754-55; J00252-54; M1S641-42. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CCTATGAACTGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CCTGTGGGGGAGACAACAGTAGAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GGGCCCCTATACTGGTCATCTATGATAGTGACCGGCCCTCAGGGATCCCTGAGCGAT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 ACTCCCCTGTGCTGGTCATCTTTCAAGATAGCAAGCGGCCCTCAGGGATCCCTGAGCGAT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCTGGCTCCAAATCAGGGAACACCCCCCCTGACCATCAACGGGGTCGAGGCCGGGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 TCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGGACCCAGGCTATGG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAGGCTGACTATTACTGTCAGGTGTGGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGACCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCCTCCTCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCATAAGTGACT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 CCTGCTCTGGAGATACATTGGGGGATAATATGCTTGCTGGTATCAGCAGAAGCCAGGCC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81. .399
/gene="immunoglobulin lambda light chain"
                                                                                                                                                                                                                                                                                                                                         'gene="immunoglobulin lambda light chain"
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/gene="immunoglobulin lambda light chain"
                                                                                                                                                                                                                                                                                                                                                                                             gene="immunoglobulin lambda light chain"
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                                                                                                                                                                                                                                    /cell_type="B-cell"
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1. 725
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                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /proteIn_id="CAA40940.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="constant region"
226 c 199 g 1
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400. .719
                                                                                                                                                                                              chromosome="22"
                                                                                                                                                                                                                    clone="cML23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STVEKTVAPTECS"
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Matches 576; Conservative
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/product="Unknown (protein for MG:40425)"
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a 277 c 219 g 164 t
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                                                                                                                                                                                                                                                                                                             566 GAGACCACCACCCTCCAAACAAAGAACAACAAGTAAGGGGGGGCAGCAGCAGTATCTGAGC 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGCTGACTACTATTACTCATCAGACAGTAGTAGTATCATTGGGTGTTCGGCGGA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 GGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTGTTCCCG 445
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                                                                                                                                                                                                                                                                                                                                                                                124 TGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCGGGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                184 GCCCCTATACTGGTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGGCTCCAAATCAGGGAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGGGAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGACCCGGGTGACCGTCCTAGGTCAGCCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTC 483
                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                       26 AIGGCCIGGACCCCTCTCTGCTCCCCCTCCTCTTTCTGCACAGTCTCTGAGGCCTCC 85
                                                                                                                                                                                                                                                 4 AGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCCAGGTGCACGATGTGCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.1%; Score 522.4; DB 9; Length 890; Best Local Similarity 84.1%; Pred. No. 1.6e-117; Matches 589; Conservative 0; Mismatches 111; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCAT 703
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ORIGIN
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Search completed: April 6, 2003, 01:55:54 Job time : 2214.18 secs

Sequence:

Run on:

Searched:

Database

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ALIGNMENTS
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AAX06951
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AAS22482
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1 ATGAAACACCTGTGGTTCTT......CCCTGTCTCCGGGTAAATGA 1431
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                                                                                               2 DNA sequences (AAT62509 and AAT62510) respectively code for primatised forms (AAW01817 and AAW01818) of the light and heavy chain of cynomologue (AAW01817 and AAW01818) of the light and heavy chain compains monkey anti-human B7. artigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes are inserted into heavy chain constant region of NEOSFLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7. I antibody shave also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                  for treating autoimmune disease or graft-versus-host disease
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Best Local Similarity 100.0%; Pred. No. 1.1e-276;
Matches 1431; Conservative 0; Mismatches 0; Indels 0;
                                  Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host di
                                                                                                                                                                                                                                                        Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;
                                                                           Claim 7; Fig 8B; 81pp; English
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1997-108638/10.
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Monoclonal antibody, Mab, macaque, heavy chain, primate, antigen, CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; 88.
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/product= 7C10 heavy chain
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New monoclonal antibodies specific for B7.1 or B7.2 antigens and hinkibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                             Example 7; Fig 3b; 87pp; English.
                                                         (IDEC-) IDEC PHARM CORP
                                                                      Anderson DR, Brams P,
                                                                                    WPI; 1998-286601/25.
P-PSDB; AAW63761.
                            29-OCT-1997;
                                           08-NOV-1996;
               14-MAY-1998
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Hanna N;

97WO-US19906 96US-0746361 This sequence encodes a primatized form of the

from macaque. This sequence is used in a method which studies new conclored antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28 Such Mab's are specific immunosuppressants for treatment of diseases involving of T cell'B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins induces long-term antigen-specific immunosuppression, i.e. it inhibits production of interleukin. 2 (IL-2), T cell proliferation and inhibits antigen-specific immunoglobulin G (IgG) responses. antibody 7C10 heavy chain

Sequence 1431 BP; 322 A; 469 C; 380 G; 260 T; 0 other;

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RESULT 3 AAS17243

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Human, macaque monkey; light chain; primatised antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; bp. 1 antigen; CD80; B. 2 antigen; CD86; B. cell cancer; metastasis; tumour; B. cell lymphoma; B. cell leukaemia; autoimmune disease; graft-ve-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
                                                                                                                                                                             DNA sequence of a primatised form of the heavy chain of 7C10 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Heavy chain of 7C10 antibody"
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is conservation to the apoptosis of B7+ cells. The invention is a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell lymphoma, B cell lymphoma, B cell lymphoma, a systemic lupus, erythematosus, cidiopathic thrombocytopenia purpura, systemic lupus, erythematosus, cidiopathic thrombocytopenia purpura, systemic lupus, erythematosus, crype I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allersy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive disease and ulcerative colitis, food-related allergies e.g. magraine, chinitis and eczema, and other types of allergies. The present nucleic solitis collision of inhibit production of the collision of inhibit production of interleukin-2 (IL-2)

Gaps Score 1431; DB 24; Length 1431; Pred. No. 1.1e-276; ; 0 .. 0 0; Mismatches 100.0%; Best Local Similarity 100.0 Matches 1431, Conservative Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primarised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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                                                       Score 1315.8; DB 18; Length 1431;
Pred. No. 1.1e-253;
0; Mismatches 72; Indels 0;
                                                                                       ;
                                                                                                               1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCCT
                             Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
and graft-versus-host disease.
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95.0%;
                                                                                  Matches 1359; Conservative
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Best Local Similarity
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                                      1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCC
                                                                           CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTTGACTCAAAGGC
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This sequence encodes a primatized form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such MAb's are specific immunosuppressants for treatment of diseases involving to cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, theumatory bowel disease, allergy and multiple sclerosis, graft vs. Inflammatory bowel disease, allergy and multiple sclerosis, graft vs. con check of the properties of the stand of the properties of the stand of the stand of the same optionally combined with other proteins and induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and entigen-specific immunoslobulin G (IgG) responses.
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91.9%; Score 1315.8; DB 19; Length 1431;
Best Local Similarity 95.0%; Pred. No. 1.1e-253;
Matches 1359; Conservative 0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
e.g. graft rejection or tumours
                                                                                                  Example 7; Fig 5b; 87pp; English.
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/\*tag= a /product= "Heavy chain of 16C10 antibody"

<u>ن</u> Brams

Hanna N,

Anderson DR,

WPI; 2002-089895/12. P-PSDB; AAU11646.

2000US-0576424.

22-MAY-2000;

(IDEC-) IDEC PHARM CORP

22-MAY-2001; 2001WO-US16364

WO200189567-A1

29-NOV-2001.

Location/Qualifiers

Key

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             GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA
                                                                                 CCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
                                                                                                CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTC
                                                                                                                                                                    GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAAGACAAAGCCG
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                                                                                                                                        CGGGAGGAGCAGTACAACAGCACGTACGTGGTCAGCGTCCTCACCGTCCTGCACCAG
                                                                                                                                                                                                                                                       GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
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Human; macaque monkey; light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
                                                                                                                         DNA sequence of a primatised form of the heavy chain of 16C10 antibody.
                                     BP.
                              AAS17247 standard; DNA; 1431
                                                                                        12-MAR-2002 (first entry)
                                                              AAS17247;
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Chimeric - Homo sapiens. Chimeric - Macaca sp. Synthetic.

ccadddaaddccrcdacrcdarrcdaracrachacrachddaacaccracrac AATCCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 61 61 121 121 181 181 241 241 원 ઠે 유 ò 요 ò g ò g

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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is cancer treating diseases auch as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, C cancer where B cells promote the growth and/or metastasis of tumours, C cancer where B cells promote the growth and/or metastasis of tumours, C cancer where B cells promote the growth and/or metastasis of tumours, C type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple solarosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative airways disease, intestinal inflammations and allergies e.g. Crohn's calrays disease, intestinal inflammations and allergies e.g. migraine, confinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the heavy chain of 16Cl0, a primatised antibody incolinitis. Incolinitis and inhibit production of incolinitis. ö Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as GIGAAGCIGCAGCAGGGGGGAAAGGACTICTGCAGCCTITCGGAGACCCTGICCCGCACC 120 120 180 240 240 0; Gaps 9 1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCCTGTCCCAG TGCGTTGTCTCTGGTGGCTTCAGCGGTTACTACTGGACCTGGATCCGCCAGACC CCAGGGAGGGACTGGAGTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC dráckácháckásáktrasásákorasataskáskornosakakorononosak TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGATGGCTGGGGCTGGATCCGCCAGCCC 91.9%; Score 1115.8; DB 24; Length 1431; 95.0%; Pred. No. 1.1e-253; ive 0; Mismatches 72; Indels 0; 0 Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other; Example 8; Fig 5b; 89pp; English. Best Local Similarity 95.0 Matches 1359; Conservative Query Match allergy ò

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ATCGAGAAAACCATCTCCAAAGCCCAAAGGCCAGCCCCGAGAACCACCACGTGTACACCCTG 1140
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   CTGAACTTGAATTCTGTGACCGACGCGGACACGCCCTCTATTACTGTGCGAGAGGCCCT 360
                                                                       CGCCCTGATTGCACAACCATTTGTTATGGCGGCTGGGTCGATGTCTGGGGGCCCGGGAGAC 420
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Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis; treatment; prevention; cell proliferation; immune system disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a cDNA encoding an immune system molecule, ISMO-2 from an Incyte clone 2849752 isolated from the human breast tumour cDNA library (BRSTTUT13). This sequence is expressed in several libraries, generally those associated with cancer, cell proliferation, immune response or trauma. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with the immune system and
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homology to vertebrate
heavy-chain"
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432..473
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                                                                                                                                                                        Human immune system molecule, ISMO-2 cDNA.
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78..1490
                                                                                                                                                                                                                                                                                                      "ISMO-2"
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P-PSDB; AAY44721.
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                                                                                                           GTGAAGCTGCAGCAGTGGGGCGAAAGACTTCTGCAGCCTTCGGAGACCCTGTCCCGCACC
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65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.
1139 CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT 1198
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                                                  GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACTGGCTGAAAGG
                                                                                       CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGGAGCAATGGGCAGCCGGAGAACAACTA
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(TANA/) TANAKA H.
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or a can be New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPs). These can used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, system associated protein; HISAP-4; immune disorder; Human immune system associated protein HISAP-4 coding sequence. Baughn MR Guegler KJ,

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                                                                       Score 1234.8; DB 22; Length 1567;
Pred. No. 1.6e-237;
0; Mismatches 87; Indels 15; G
                                                 Sequence 1567 BP; 346 A; 503 C; 428 G; 289 T; 1 other;
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                                                                       Query Match
Best Local Similarity 92.9%;
Matches 1332; Conservative 0
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Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; heavy chain; gamma 1; variable region; insect host cell; baculovirus; recombinant production;
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                                          CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC
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/product= heavy_chain
/note= "constructed from PCR fragments coding for
human gammal heavy chain constant region
and the variable region from anti-rheaus
antibody D7C2"
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mouse VH gene signal sequence"
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/*tag= a
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CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAAGCA
                           GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG
                                                                                                      GGGGACCGTCAGTCTTCCTCTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG
                                                           GAGCCCAAATCTTGTGACAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG
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                                                                                                                                                         The human monoclonal antibody D7C2, of isotype 1gM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence encodes a recombinant IgM-D7C2 heavy chain fused to a mouse VH signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGGAAGTATCATGGGGACTGGTTCGACCCTGGGGCCAAGGTACCACTGTCACCGTC
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                                                                                                                                                                                                                                                                                                   DB 17; Length 1418;
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                                                                                         Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing
                                                                                                                                                                                                                                                                                                Query Match
85.4%; Score 1221.6; DB 17; Length
Best Local Similarity 92.9%; Pred. No. 7e-235;
Matches 1317; Conservative 0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                           Sequence 1418 BP; 333 A; 458 C; 378 G; 249 T; 0 other;
                                   ပ်
                                   Margaritte
                                   Kaczorek M,
                                                                                                                                     Claim 1; Page 35-37; 46pp; French
                                                                                                                haemolysis in new-born babies
(INSP ) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE.
                                  Edelman L,
                                                       WPI; 1996-162018/17.
P-PSDB; AAR93166.
                                  Chaabihi H,
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                                                                                                                                                                                                                                                                                                                                                                                   GGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG
                                                                                                                                              841 ACCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCCACGAAGACCCTGAGGTCAAGTTC
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Best Local Similarity 90.0%; Pred. No. 7.4e-225;
Matches 1288; Conservative 0; Mismatches 116; Indels 27;
                                                                                                                                                            Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
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P-PSDB; AAW14925.
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DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAM14925), gamma-4E carrying the L236E mutation (AAM14926) and gamma-4PE (AAM14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4, E and CE9 gamma-4PE, in which the human IgG4 Fc binding domain framework is combined with the antigen binding domains (see also AAM14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis. Disclosure; Page 91-93; 155pp; English.

Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;

7 180 300 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGTCCCGCACC 120 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTACTGGACCTGGATCCGCCAGACC 180 240 240 300 360 Gaps 9 9 1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG CCAGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC CTGAACTTGAATTCTGTGACCGACGCGGACACGCCGTCTATTACTGTGCGAGAGGCCCT AATCCCTCCTCAAGAGTCGAGTCACATTTCAAAAGACACGTCCAAGAACCAGTTCTTC AATCCCTCCAACAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC DB 18; Length 1404; 27; Query Match

81.6%; Score 1168.2; DB 18; Length
Best Local Similarity 89.9%; Pred. No. 3.2e-224;
Matches 1286; Conservative 0; Mismatches 118; Indels 121 241 61 181 181 241 301 301 8 a ò ò 셤 g g ò ò ò ò

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mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4F. (DE9 gamma-4F and CE9 gamma-4F, in which the human IgG4 FC binding domain framework is combined with the antigen binding domains (see also AAM14922-23) of macaque anti-human CD4 monoclonal antibody E9-1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4B and -4PE mutations confer activity enhanced stability and aliminate depleting activity. The antibodies can be used to treat
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Pred. No. 6.7e-224;
0; Mismatches 119; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                     CD4; monoclonal antibody; chimaeric antibody; recombinant an eynomolgue monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma-4E; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;
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                                                                                    AATCCCTCCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC
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The present sequence encodes a single chain antibody of the invention. The specification describes a substance can inhibit the binding between hepatitis C virus (HCV) and cells with potential HCV infection, cells with expression of CD81, or CD81. This substance is especially an antibody with affinity towards HCV BZ/NS1 protein, containing amino acid sequences based on the complementarity determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable regions. The antibody inhibits the viral envelope GJycoprotein. It is also a CD81 inhibitor. The antibodies and drugs are used for treatment and/or prevention of hepatitis C, or for diagnosis of hepatitis C.
1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
                   Complementarity determining region; CDR; single chain antibody; SCFv; hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein; envelope glycoprotein; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remedies for hepatitis C containing substances with antiviral effects e.g. antibodies, proceins, sulfated polysaccharides and low-molecular compounds, by inhibiting binding of hepatitis C virus envelope glycoprotein or CD81 -
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product= "single chain antibody"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 41; Page 105-108; 138pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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P-PSDB; AAG63640.
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Query Match 79.3%; Score 1135; DB 22; Length 1428; Best Local Similarity 87.6%; Pred. No. 1.4e-217; Matches 1253; Conservative 0; Mismatches 175; Indels 3;

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                   anti-RSV F-protein hMAbs for use in the treatment RSV infection.
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Pred. No. 1.2e-215;
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The transfected host cells provide a constant,
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                                                                                       Seguence 1428 BP; 326 A; 465 C; 372 G; 265 T; 0 other;
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Human monoclonal antibody specific for respiratory syncytial virus fusion protein - used for the prevention and treatment of RSV
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                                                                                                                                                                                   AAGACCACGCCTCCCGTGCTGGACTCCGACGCTCCTTCTTCTACAGCAAGCTCACC
                                                                                                                                                                                                                                                                                GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT
                                                                                            TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
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                             CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTGGTCAAAGGC
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ISM Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria; Primates; Catarrhini, Hominidae, Homo.
CE 1 (bases 1 to 1020)
RS NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov/
Tissue Procurement: Low Standt
CONA Library Presparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2094 row: h column: 21
High quality sequence start: 21
High quality sequence start: 21
High quality sequence stop: 681.
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BQ709771 AGENCOURT
BQ706140 AGENCOURT
BG755166 602711488
BM007892 603617577
BQ708857 AGENCOURT
                                                                                                                                                   April 5, 2003, 19:13:54 ; Search time 2723.68 Seconds (without alignments) 8508.978 Million cell updates/sec
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                                                                                                                                                                                                                                                                                               1 ATGAAACACCTGTGGTTCTT......CCCTGTCTCCGGGTAAATGA 1431
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                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                  16154066 segs, 8097743376 residues
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Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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756 CAGCGACATCGCCGTGGAGTGGGAGTGGGCAATGGGCAGCCGGNAGAAACTACTACTAGACC 815
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KEYWORDS
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/tissue_type="lymphoms.cell line"
/lab_hogt=="but by page-resistant")
/lab_hogt=="but by page-resistant")
/note="Organ: lymph, vector: poffB7; Site_1: XhoI; Site_2:
/note="Organ: lymph, vector: poffB7; Site_1: XhoI; Site_2:
/note="Organ: lymph, vector: poffB7; Site_1: XhoI; Site_2:
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/note_Town made by oligo-dT priming_Directionally cloned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTCGACAAAGGCTTCTATCC 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 GACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGGTGTCGTGGAACTCAAGCGCCCTGACCAGCGGCGTGCACACTTCCCGGCTGTCCT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 ACAGTCCTCAAGACTCTACTCCCTCAGCGGGGGGGGGCGTGCCCTGCCAGCAGCTTGGG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAA 728
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                              /organism="Homo sapiens"
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/clone="IMAGE:5924420"
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Email: cgapbs-rémail.nih.gov
Tisaue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov m column: 16
High quality sequence start: 3
High quality sequence stop: 675.
Location/Qualifiers
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1 (bases 1 to 947)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
1267 ACGCCTCCCGTGCTGGACTCCGACGCTCCTTCTTCTTCTTCACAGCAAGCTCACCGTGGAC 1326
                                                                                                                                                                                                                                        1327 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1396
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1 (bases 1 to 958)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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            429 GCACGTACCGTGTGGTCACCGTCCTCACCGTCCTGCACCAGGACTGGCTGATGGCAAGG 488
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                                                   AATCTIGIGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGAC 799
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
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DNA Sequencing by: Agencourt Bioscience Corporation
follone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLGMA464 row: a column: 01
High quality sequence stop: 705.
Location/Qualifiers
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1 (Dases 1 to 901)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/db xref="Laxon:9606"
/clone="InAGE:4852076"
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602711488F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 926)

                                                                                                                                                                                                                             1338 GCAGCAGGGAACGICTICTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 1397
   1218 CGCCGTGGAGTGGGAGAGCAATGGCCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT 1277
                                                                                                                 1278 GCTGGACTCCGACGGCTCCTTCTTCCTCACAGCAAGCTCACCGTGGACAAGAGCAGGTG 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Studt, M.D., Ph.D.
Tissue Procurement: Louis M. Studt, M.D., Ph.D.
Tissue Procurement: Louis M. Studt, M.D., Ph.D.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov o column: 21
High quality sequence stop: 888.
Location/Qualifiers
                                                                                                                                                                                                                                                                  731 GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGGTG 790
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                              671 CGCCGTGGAGTGGGAGGAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT
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                                                                                                                                                                                                                                                                                                                                               1398 GCAG-AAGAGCCTCTCCCTGTCTCCGGGTAAA 1428
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/db_xref="texaon:9Gpf0" |
/clone="IMAGE:545061" |
/clone="IMAGE:545061" |
/clone="IMAGE:545061" |
/clone="IMAGE:131" |
/lab host=="DHIOB (phage-resistant)" |
/lab host=="DHIOB (phage-resistant)" |
/not=="Ocgan: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/AhoI sites using the following 5: adaptor:
GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library." |
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Email: cgapbs-r@mail.nih.gov
fissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1939 row: j column: 20
High quality sequence stop: 834.
Location/Qualifiers
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/organism="Homo sapiens"
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988 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8352194 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277561
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NH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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/db xref="raxxn:9606" / clone="MAGE:5924769" / clone="IMAGE:5924769" / clone="IMAGE:5924769" / clone="IMAGE:5924769" / clone="IMAGE:5924769" / clone="IMAGE:99" / clone="IMAGE:99" / clone="IMAGE:99" / clone="IMAGE:99" / clone="IMAGE:99" / clone="IMAGE:99" / clone="IMAGE:99" / clone="IMAGE:"DANA made by oligo-dT priming. Directionally cloned into EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI; xDNA made by oligo-dT priming. Directionally cloned into EcoRI; xDNA made by oligo-dT priming. Site_2: GGCACGAG(G). Size-selected >500bp for average insert size in .8bb. Library constructed by Ling Hong in the laborarorry of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript IN RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLCM2095 row: g column: 10
High quality sequence stop: 723.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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tive 0; Mismatches 18;
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/clone='Indage:6281659"
/clone='Indage:sapient'
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
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AGENCOURT 8443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
AGENCOURT 6443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
BQ711255
BQ711255.1 GI:21850154
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1 (bases 1 to 887)

NIH-MGC bttp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                    1023 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGAGCCCTCCCAGCCCCAT 1082
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM244 row: m column: 20
High quality sequence stop: 681.
                                                                                                                                                                                                                                                                                                          484 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA 543
                                                                                       784 GAACACGCCTCCCCGTGGACTCCGACGGCTCCTTCTTCCTCTACAGGAAGCTCACC 843
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Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: FooRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies). Note: this is a
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCWA469 row: i column: 20
High quality sequence stop: 667.
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1 (bases 1 to 995)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1178 GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT-GGAGTGGGAGAGC
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BQ711291 RRNA linear EST 16-JUL-2002 AGENCOURT\_8347186 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6279096

DEFINITION

BQ711291 LOCUS

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/db_xrefa="taxnon" dgf6"
/clone="IMAGE:6279066"
/clone="taxnon" dgf6"
/clone="taxnon" dgf6"
/clone="taxnon" dffage=resistant)"
/lab_host="DH10B (pfage=resistant)"
/lab_host="DH10B (pfage=resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EccR1; CholM made by 0.1go-dT priming. Directionally cloned into EccR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Garald M. Rubin (University of Callifornia, Barkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supergript II RT (Life Technologies). Note: this is a
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                                                                                                         Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 881) NIH-MGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2468 crow: c column: 01
High quality sequence stop: 721.
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                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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Matches 810; Conservative
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AGENCOURT 8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
5', mRNA Sequence.
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                                               DB 14;
                                               Query Match 55.9%; Score 800.2; DB 14; Best Local Similarity 94.4%; Pred. No. 2.2e-180; Matches 840; Conservative 0; Mismatches 49;
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| Corganism="Homo sapiens"
| Ab xref="taxon:9606" |
| Ab xref="taxon:9606" |
| Ab xref="taxon:9606" |
| Alone=lib="NIH MGC 99" |
| Alone=lib="NIH MGC 99" |
| Alab-hogi="DHINB (phage-resistant)" |
| Alab-hogi="Umphi, Vector: pOTBY; Site 1: Xhol; Site 2: FOORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGAGAGG): Size-selected >SOODp for average insert size into EcoRI, size-selected >SOODp for average insert size of Gerald M. Rubin (University of California, Berkeley) using ZAR-CDNA synthesis kit (Stratagene) and Superscript Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUOSTRE 6887080 NIH_MGC_99 Homo saplens cDNA clone IMAGE:5929343
57, mRNA gequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1031)

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1032 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGGCCCCCATCGAGAAAAC 1091
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2107 row: e column: 24
High quality sequence stop: 573.
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                                                                                                                                                                                                                                                                                                                                            NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
               421 TGGCAAGGAGTACAAGTGCAAGGTCTCCCAACAAAAAGCCCTCCCAGCCCCCCATCGAGAAAAC
                                                                                               481 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
                                                                                                                                CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC
                                                                                                                                                                                                                  601 CGACATCGCCGTGGAGTGGGAGGAATGGGCAGCCGGAGAACAACTACAAGACCACCCC
                                                                                                                                                                                                                                                            TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG
                                                                CATCTCCAAAGCCAAAGGCCCCCCAAAACCACAGGTGTACACCCTGCCCCCATCCCG
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609

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GGACGAG(G). Library constructed by Ling Homg in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emall: Gapbs-radmail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencult Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lull.gov

Plate: LLCM2382 row: K column: 20

High quality sequence stop: 619.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 936)

S NHH-MGC http://mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

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Email: cgapbs-r@mail.nih.gov
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Location/Qualifiers

Location/Qualifiers
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 Length 940;
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Pred. No. 2.1e-179;
0; Mismatches 5;
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Best Local Similarity 99.3%;
Matches 810; Conservative
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammália; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BQ710532.1 GI:21849431 EST.

human.

ORGANISM

VERSION KEYWORDS SOURCE

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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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4 TGAGGCTCTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAATGA 1431	1374	ò
B GCTCACCGTGGACAAGAGCAAGGGGGAACGTCTTCTCTTTCTCTGTGTGCA 897	838	qq
4 GCTCACCGTGGACAAGAGCAGGTGGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA 1373	1314	ò
9 CAACTANCAGACCACCACCATCCCATGCTGGACTCCGACGGGCTCTTTCTCCCTCTACAGG-A 837	779	qa
4 CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAA 1313	1254	δ
9 AAAGGCTTCTACCCCAGCGACATCTCCCCGTGGAGTGGGGAGAATGGGGCAATGGGCAGCCGGAGAA 778	719	qq
1195 AAAGGCTTCTATCCCAGCGACATC-GCCGTGGAGTGGGAGCGATGGGCAGCGGGGAGAA 1253	119	ò
9 ACCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTG	629	qq
5 ACCCTGCCCCATCCCGGGATGAGCTGACCAGGTCAGCCTGACCTGCCTG	1135	δ
9 GCCCCCATCGAGAAAACCATCTCCAAAAACCAAAGGGCAGCCCCGAGAACCACAGGGTAC 658	599	qa
S GCCCCATCGAGAAAACCATCTCCAAAGCCAAAAGGGCAGCCCGGAGAACCAGGTGTAC 1134	1075	δ
9 CACCAGGACTGGCTGAAGGGGTAGGAGTGCAAGGTCTCCCAACAAGGCCTCCCA 598	539	qq
1015 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1074	101	ઠે

Search completed: April 6, 2003, 06:20:24 Job time : 2734.68 secs

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

I (bases 1 to 1431)

Tanaka,S., Niwa,H. and Tanaka,H.

HUMAN MONCCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR CLONING OF GENE THEREOF

I Patent: JP 1996038178-A 20 13-FEB-1996;

TANAKA HIDEYUKI, NISSHINBO IND INC

OS Homo eaplens (human)

PN JP 1996038178-A/20

PD 13-FEB-1995

PP 20-FEB-1995

PP 19-FEB-1995

PP 21-FEB-1994

PP 19-FEB-1994

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/cell type='B cell'
1. 57
/product='signal peptide of heavy chain of human monoclonal antibody against human cytomegalovirus 65kD
1321 GTGGACAAGAGAGCAGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380
                                                                 1321 GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTTCATGCTCGTGATGCATGAGGCT 1380
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CDNA encoding heavy chain of human monoclonal antibody against
human cytomegalovirus 65kD antigen.
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                                                                                                                                      1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
                                                                                                                                                                   1381 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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/db_xref="taxon:9606"
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hypothetical: No;
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KEYWORDS
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TITLE
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qa	Db 1075 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA	GAACCACAGGTGTACACC 1134
ογ	Qy 1138 CTGCCCCATCCCGGGATGASCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAA	TGACCTGCTGGTCAAA 1197
ପ୍ର	1135	rgaccrecregrana 1194
'n	Qy 1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGGAGCAATGGGCAGCCGGAGAACAAC	GGCAGCCGGAGAACAAC 1257
qa	1195	GCAGCCGGAGAACAAC 1254
ογ	Oy 1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTC	TCCTCTACAGCAAGCTC 1317
qq	1255	rccrcracaccacic 1314
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δy	Qy 1378 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 14	CGGGTAAATGA 1431
qq	1375	cecinaarea 1428
RES AR1 LOC	1567 bp	linear PAT 16-JUN-2001
ACC	DEFINITION SEQUENCE 17 From patent US 6135941. ACCESSION AR13359 GI:14476031 VERSION AR135359.1	
SOU	KEYWORDS	
REF A	Unclassified.  REFERENCE 1 (bases 1 to 1567)  AUTHORS Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,	, Au-Young, J.,
H D	TITLE Human immune system associated molecules JOURNAL Patent: US 6135941-A 17 24-OCT-2000;	
FEA	SALUKES	
BAS	BASE COUNT 346 a 503 c 428 g 289 t ORIGIN	1 others
Oms	Query Match Best Local Similarity 92.9%; Pred. No. 2.8e-240 Matches 1332; Conservative 0; Mismatches 87	; Length 1567; Indels 15; Gaps 3;
<i>₹</i> 0 €	1 ATGAAACACCTGTGGTTCTTC 	GATGGGTCCTGTCCAG 60
ò	61	AGACCCTGTCCCGCACC 120
qa	Db 138 GTGCAGCTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC	AGACCCTGTCCCTCACC 197
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<b>Σ</b> Σ	AUTHORS IShbash,T. Ono,Y., W Kusano,J., W Kasano,J., W Yamsshita,H. Yamsshita,H. Yamsshita,H. Yamshita,H. Yamshita,H. Yamshita,H. Yamshita,H. Yamshita,H. Yamshita,H. Yamshita,H. Yamshita,H.		COMMENT NEDO human ci Economy, Trac Economy, Trac Research, Ass Construction Science, Univ Genome Centes full insert s Loce	Source 1.  /db /db /c1 /db /c1 /c1 /c1 /c1 /c1 /c1 /c1 /c1 /c1 /c1	ORIGIN Query Match Best Local Similarity Matches 1326; Conserv	Oy 1 ATGAAACACCTGTGC DD 36 ATGAAACACCTGTGG Oy 61 GTGAAGCTGCAGCAC	36 121 156 178 216	Qy 238 TACAATCCCTCCTC 
Db 433ATGACGTAGGTTTAAGGGGGAACTACGGTATGGACGTCTGGGGCCAGGGA 485  Oy 418 GACCTGGTCACCGTCTCCTCAGCTAGGACCATCGGTATGGACGTCTGGGGCCAGGGA 485  Db 486 ACCTGGTCACCGTCTCCTCAGCTACCACAAGGGCCCATCGGTCTTCCCCCTGGCACCC 545  Oy 478 TCCTCCAAGAGCACCTCTCGGGGCACAGGGCCCATCGGTCTTCCCCTGGCACTCTTC 537  Db 546 TCCTCCAAGAGCACCTCTGGGGGCACAGGGCCTGGGTCAGGTCATTC 537  S46 TCCTCCAAGAGCACCTCTGGGGGCACAGGGCCTGGGCTGGTCAGGTCATTC 605  Oy 538 CCCGAACCGGTGACGTGCTGGGACACAGGGCCCTGACCTGGTCAAGAACTTC 605  Oy 646 TCCTCCAAGAGCACTCTGGGGACACAGGGCCCTGACCTGGTCAAGAACTTC 505  OY 646 TCCTCCAAGAGCACTCTGGGGACACAGCGGCCCTGACCTGGTCAACACACTTC 507  OY 646 TCCTCCAAGAACCAGTGACCTTCAAGAACACACACAGGGCCTGACCTTC 597  OY 646 TCCTCAAGAACCAGTGACCTTCAAGAACACACACACACAC	598 666 658	Oy         718         GTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACGTGCCCACGTGCCCA         777           Db         786         GTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACGTGCCCA         845           Oy         778         GCACCTGAACTCCTGGGGGGACCGTCAGTTTCCTCTTCCCCCCAAAACCCAAGGACACC         837           Db         846         GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCCAAAACCCAAGGACACC         905	Qy         838         CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGACGCGTGAGCCACGAAGAC         897           Db         906         CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGAGCCACGAAGAC         965           Qy         898         CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG         957           Db         966         CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG         1025	Oy         958         CCGCGGGAGGAGGAGTACAACAACAACAACATACCGTTGGTCAGCGTCCTCCACCGTCCTGCAC         1017           Db         1026         CCGCGGAGGAGGAGTACAACAACAGCACGTCCTCCACCGTCCTCCACCGTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCACCTCTCCACCTCTCACCTCTCCACCTCTCACCTCTCCACCTCTCACCTCTCCACCTCTCACCTCTCACCTCTCCACCTCTCACCTCTCACCTCTCCACCTCTCACCTCTCACCTCTCACCTCCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCTCACCTCACCTCTCACCTCACCTCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCAC	OY         1078         CCCATCGAGAAAACCATCTCCAAAGCCAAAGGCAGCCCCGAGAACCACGGTGTACACC         1137           Db         1146         CCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC         1205           OY         1138         CTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCTGACCTGCTGGTGAAA         1197	1206 CTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCTGACCTGGTCAAA  1198 GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAACGAGCCAGCC	1258 TACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTTCTTAGAGG  [	UY 1378 GULTIBLALARICALIALARIGEGRAPAGAGCCTCTCCCTGTCTCCGGTAAATGA 1431

con and industry of Japan; cDNA full insert sequencing: sociation for Biotechnology (RAB); cDNA library is sociation for Biotechnology (RAB); cDNA library in and 5'-end one pass sequencing; Institute of Medical inversity of Tokyo, Laboratory of Genome Structure, Human et j. 3'-end one pass sequencing: RAB; clone selection for sequencing: RAB and Helix Research Institute. ., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
uta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
Watanabe,M., Fujimori,K., Tanal,H., Ishida,M.,
Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S.,
Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and 3 96 bp mRNA linear PRI 15-JUL-2002 fis, clone SYN01104, highly similar to ission 08-JUL-2002) Sumio Sugano, Institute of Medical Science, of Tokyo, Laboratory of Genome Structure, Human Genome rokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan al@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, GI:21758543 ng; fis (full insert sequence). s synovial membrane (knee) cDNA to mRNA, clone\_lib:SYN Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; utheria; Primates; Catarrhini; Hominidae; Homo. 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MONOCLONAL RECOMBINANT ANTI-RHESUS D (D7C2) ANTIBODY
PACENT: WO 9607740-A 7 14-MAR-1996;
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Other publication FR 2724182 960308.
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84.6%; Score 1210.4; DB 6; Length 1418;
Best Local Similarity 92.4%; Pred. No. 2.5e-235;
Matches 1310; Conservative 0; Mismatches 96; Indels 12; 1 (bases 1 to 1418)

Edelman,L., Margaritte,C., Kaczorek,M. and Chaabihi,H.
Monoclonal recombinant anti-rhesus D (D7C2) antibody
Patent: US 6312690-A 7 06-NOV-2001; linear DNA 253 t Sequence 7 from patent US 6312690. AR176296 Location/Qualifiers /organism="unknown" 379 g AR176296.1 GI:17918651 454 C 1418 Unclassified. 332 a Unknown. Unknown KEYWORDS SOURCE ORGANISM BASE COUNT ORIGIN DEFINITION 1407 1258 1287 1347 1378 ACCESSION VERSION TITLE JOURNAL 13 190 253 313 433 1318 133 193 493 RESULT 8 AR176296 LOCUS REFERENCE AUTHORS FEATURES ð g ò 셤 ò g ò g В ò ò 셤 ò g d ઠ 셤 ò q ద ò ò 8

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Sugano, S. and Suzuki, Y.

Direct Submission

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Direct Submission

Niversity of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8619, Japan

(E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Economy, Trade and Industry of Economy, Trade and Industry of Sagan, Construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB; clone selection for full insert sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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/db_xref="HomoTyLIGM:AKOS7775"
/db_xref="taxon:9606"
/clone="CBL03624"
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Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL clone:CBL03624.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 81.9%; Score 1171.4; DB 6; Length 1404; I Similarity 90.0%; Pred. No. 2e-227; 288; Conservative 0; Mismatches 116; Indels 27;
       1 (bases 1 to 1404)
Hanna,N., Newman,R.,Anthony. and Reff,M.Elliot.
Recombinant anti-CD4 antibodies for human therapy
Patent: US 6136310-A 7 24-0CT-2000;
Location/Qualifiers
                                                                  267
                                                       /organism="unknown"
448 c 377 g
                                                1. .1404
Unclassified
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construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB. Incation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDPLYDSHHYWAWIRQQPGKGLEWIGHINSYAYKFYNGSLESRLSMSMGTSRNDFSLK
MTGYTDVDTAAYFCALFKSTWFDPWGPGTLVIVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVUVDYPEPPYVSWNSGALTSGVHTFPAVLQSGGLYSLSSVYTYSSSLGGTOTY
ICNNAHKPSNTTWORKVEPKRGGTOTY
PEVTCVVVDVSHEDPEVKFNWYVDGYEVHNETKPREEQYNSTYRVGSYLTVLHQDRI
NGKEYKCKNSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MGHPWFFLLLVTAPRWVLSQVRLQESGPGLVKPSQTLSLTCSVS
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Pred. No. 3.8e-227;
0; Mismatches 105; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="SYNOV2001300"
/tissue type="synovial membrane tissue
                                                                                                                                                                                                                                                                         /clone_lib="SYNOV2"
/note="cloning vector: pME18SFL3"
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/note="unnamed protein product"
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/protein_id="BAC05021.1"
/db_xref="GI:21757093"
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Best Local Similarity 90.4
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Karusa-Kamatari, Kisarazu, Chiba 222-0812, Japan
(E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Innomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Mishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
NEDO human cDNA sequencing project
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK097365.1 GI:21757092 oligo capping; fis (full insert sequence). Homo sapiens synovial membrane tissue from rheumatioid arthritis CDNA to mRNA, clone_lib:SYNOV2 clone:SYNOV2001300.
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                CCGGCTGTCCTACAGTCCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCC
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1 (bases 1 to 1404)
Hanna,N., Newman,R.Anthony. and Reff,M.Elliot.
Recombinant anti-CD4 antibodies for human therapy
Patent: US 6136310-A 11 24-OCT-2000;
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Sequence 11 from patent US 6136310.
AR135377 GI:14476049
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                                                                             Length 1404
                                                                             Score 1168.2; DB 6; Length
Pred. No. 8.9e-227;
0; Mismatches 118; Indels
                                       265
Location/Qualifiers
             1. .1404
/organism="unknown"
447 c 379 g
                                                                                Query Match
Best Local Similarity 89.9%;
Matches 1286; Conservative
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<u>\$</u>	961 CGG	CGGGAGGAGCAGTACAACAGCAACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020	ð :	
		GACTGCTGAATGGCAAGGAGTACAAGGTCTCCAACAAAGCCCTCCCAGCCCC 1080	8 &	301 CTGAACT
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AR135376 LOCUS		R135376 1404 bp DNA linear par 16TIN_2001	qa	703 GACAAGA
DEFINITION ACCESSION			ò	781 CCTGAAC
VERSION KEYWORDS		R135376.1 GI:14476048	qq	754 CCTGAGT
SOURCE	MSIN	Unknown. Unknown.	ò	841 ATGATCT
REFERENCE		nclassified. (bases 1 to 1404)	q	814 ATGATCT
AUTHORS TITLE		Hanna, N., Newman, R. Anthony. and Reff, M. Elliot. Recombinant anti-C14 antibodies for human therapy	ò	
FEATURES	, (	acent: US 6136310-A 9 24-OCT-2000; Location/Qualifiers	qq	
	Bource	11404 /organism="unknown"	ò	961 CGGGAGG
BASE COUNT ORIGIN	INOC	313 a 446 c 379 g 266 t	QQ	934 CGGGAGG
Quer	y Match	81.5%;	δλ	1021 GACTGGC
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GSLRAEDFWAYYCARGYSTRAAALIKYNEDSWGGTLVYTVSSASTKGPSVFPLAPSSK
STSGGTAALGGLVKDY FPEPYTVSKNSKGATHTFDPALLQSSGLYSLSSVYTVPSS
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TCLIKKGFYPSDIAVENSKNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHBALHNHYTQKSLSLSPGK"
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Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
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Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A.,
Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K.,
Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y.,
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Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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Isogai, T. and Yamamoto, J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1633;
Query Match 78.7%; Score 1125.8; DB 9; Best Local Similarity 88.1%; Pred. No. 3.5e-218; Matches 1249; Conservative 0; Mismatches 162;
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189 CCAGGGAAGGGCTGGAGTGGATTGGGGAAATCATTCATCATGG---AAACACCAACTAC
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1 (basea 1 to 1507)

Kusunoki,C. and Fukushima,A.

Process for producing monoclonal antibody

Patent: 19 2000342279-A 1 12-DEC-2000;

JAPAN TOBACCO INC, ABGRIX INC

OS Homo sapieng (human)

PD 12-DEC-2000

PP 30-MAR-2000 JP 2000097874
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CIZN15/09,CIZN1/15,CIZN1/19,CIZN1/21,CIZN5/10,CIZN15/02,
11/08//
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Pred. No. 7.4e-218;
Mismatches 108; Indels 42;
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Best Local Similarity 89.5%;
Matches 1281; Conservative (
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Sequence Sequence Sequence

110, App 110, App 4, Appli 3, Appli

Sequence Sequence

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Sequence 2, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONEX MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
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ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-UNV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acid
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100.0%; Pred. No. 9.9e-103;
iive 0; Mismatches 0;
US-08-899-575-153

US-08-899-575-153

US-08-89-90-75-153

PCT-US94-07659-4

US-07-690-192-2

US-08-487-550-6

US-08-487-550-6

US-08-476-3494-110

US-08-476-3494-110

US-08-559-372A-10

US-08-646-981-3

US-08-646-981-3

US-08-43-439-58

US-09-423-439-58

US-09-421-439-58

US-09-421-439-58

US-09-421-439-58

US-09-421-439-58

US-09-478-039-11

US-08-478-039-11
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F: 699 Prince Street
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 234; Conservative
     MOLECULE TYPE: protein
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STREET: 69
CITY: Alex
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Sequence 170, App
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Patent No. 5189147
Sequence 9, Appli
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                                                                                                                                                           March 29, 2003, 09:06:24 ; Search time 8.31417 Seconds
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  828.100 Million cell updates/sec
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1243
1 MRVPAQLLGLLLLWLPGARC......CQVTHEGSTVEKTVAPTECS 234
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                         GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-08-497-550-10
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US-08-751-359-22
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Sequence 10, Application US/08487550
Sequence 10, Application US/08487550
Sequence 10, Application US/08487550
Sequence 10, Elia 898
TITLE OF INVENTION: MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRINATIZED FORMS THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PCTAPKLLIYDINKRPSGISDRPSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRVPAQLIGILILIMIPGARCESVITQPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRVPAQLIGLILIMIPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 236;
186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22314
ZIP: 22314
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLESSIFICATION: 435.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.3%; Score 973; DB 3; Best Local Similarity 80.1%; Pred. No. 8.3e-79; Matches 189; Conservative 13; Mismatches 32
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Sequence 7, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-836-2021
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-487-550-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-049-672A-7
                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
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61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                           61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                GGTRVTVLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
                                                                                                                                            121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LIGLIAHFTDSA-ASYELSÓPRSVSVSPGOTAGFTCGGDNVGRKSVOWYOOKPPOAPVLV 65
                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08523894

Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
COTY: ADALAGAMATIA
                                                                                                                                                                                                                               181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                   181 VETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Alexandria

COUNTY: VA

COUNTY: USA

ZIP: 22314-3187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,894

FLING DATE: 06-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: TESKIA, ROBIN L.

REFISHANIN: NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 35,030

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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86.0%; Pred. No. 1.4e-82;
tive 10; Mismatches 21;
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.0%
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 233 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein
US-08-523-894-6
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                                                                                                                                                                                                                                                                                                                               RESULT 2
US-08-523-894-6
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us-09-758-173-2.rai

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TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 235 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: THYRNOT10
; CLONE: 2872705
US-09-049-672A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                      STATE: C. COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 RVTVLGOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LLGLLLLMLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR---NEYVHWYQQKPARAP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LLLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Bughn, Mariah R.
APPLICANT: AMERICAN: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 TIPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
70.8%; Score 880.5; DB 4;
Best Local Similarity 74.9%; Pred. No. 1.3e-70;
Matches 173; Conservative 17; Mismatches 38;
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                  Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REPERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                              ADDRESSEE: Incyte Pharmaco
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LIBRARY: ADRETUTOS
; CLONE: 2492122
US-09-049-672A-7
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                                                                                                                                                                                                                                                                USA
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STRANDEDNESS:
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58 KPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHP 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Goraley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.8%; Score 867.5; DB 4; Length 235; Best Local Similarity 74.7%; Pred. No. 1.8e-69; Matches 177; Conservative 16; Mismatches 29; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DOS
SOFTWARE: FeatSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-378-939-12; Sequence 12, Application US/08378939; Patent No. 5876961; GENERAL INFORMATION:
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; Sequence 10, Application US/09049672A; Patent No. 6135941; GENERAL INFORMATION:

RESULT 5 US-09-049-672A-10

APPLICANT: Hillman, Jennifer L.

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VTLFPPS------SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 GARCAYELTOPPSYSYSPGOTARITCGGDNSRNEYVHWYQOKPARAPILVIYDDSDRPSG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baugh, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 SKOSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

68.8%; Score 855.5; DB 4;
Best Local Similarity 73.2%; Pred. No. 2.2e-68;
Matches 167; Conservative 14; Mismatches 32;
                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #
APPLICATION NUMBER: US/08/793.450
FILING DATE: 03-MAR-1997
CLASSIFICATION DATA:
PRICING DATE: PS-1994
ATTORNEY/AGENT INPORMATION:
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMUNICATION INFORMATION:
TELEPRAX: 703-413-3000
INFORMATION FOR SEQ ID NO: 6:
SEGURENCE CHARRATERISTICS:
LENGTH: 238 minto acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09049672A Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L. APPLICANT: Lal, Preeti APPLICANT: Tang, Y. Tom APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
TOPOLOGY: ):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-793-450-6
                                                                                                   ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
             STREET: LICTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
                                             STATE: VA
COUNTRY: USA
22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-049-672A-12
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 APKIMIYEVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCCSY-AGSYTVVFGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ALLLTLILTQDTGSWAQSALTQPASVSGSPGQSITISCTGTNNDVGSYNLVSWYQQHPGK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AQLIGILILMIPGARCAYELTQPPSVSVSPGQTARITCGGDNS---RNEYVHWYQQKPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 ETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BELEMAN, LENA
APPLICANT: CACZOREK, MICHEL
APPLICANT: CACZOREK, MICHEL
APPLICANT: CHAABILH, HASSAN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Indels
                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.3%; Score 861; DB 2; Best Local Similarity 75.1%; Pred. No. 6.9e-69; Matches 175; Conservative 16; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,377
REGISTRATION NUMBER: 30,377
REFRENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-378-939-12
                                                                                                                                                                                                              ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                       D. C.
U.S.
                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-08-793-450-6
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Gaps

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180 SSPVKAGVETTTPSKOSNNKYAASSYLSLTPEOWKSHKSYSCOVTHEGSTVEKTVAPTEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 WYQQKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 SDHPVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SGSWVFGGGTKLSVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 SSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTEC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRVPAQLLGLLLLWL----PGARCAYELTQPPSVSVSPGQTARITCG---GDNSRNEYVH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSVPTMAMMMLLLGLLAYGSGVDSQTVVTQEPSFSVSPGGTVTLTCGLSSGSVSTSNYPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.9%; Score 844; DB 4; Length 240; 71.4%; Pred. No. 2.3e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-152-060-70

Sequence 70, Application US/09152060

Sequence 70, Application US/09152060

Parent No. 6448230

GENERAL INFORMATION:

APPLICANT: Rosen et al.

FILE DE INFORMATION:

FILE REFERENCE: PZ003P1.US

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER PILING DATE: 1998-03-12

EARLIER PILING DATE: 1998-03-12

EARLIER PLING DATE: 1998-03-12
                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                           NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERNCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-655-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 240 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.9
Best Local Similarity 71.4
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: LNODNOT08
CLONE: 3056213
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            Palo Alto
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                                                 USA
                                                                 94304
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                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLGLLLLWLPGARCAYELTOPPSVSVSPGOTARITCGG--DNSRNEYVHWYQOKPARAPI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LLLALLTHCAGSWAQSVLTQPPSASGTPGQRVTISCSGTTSNIASNSVHWYQLVPGAAPK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 TPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 TPSKOSNNKYAASSYLSLTPEQWKSHKSYSCOVTHEGSTVEKTVAPTECS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.8%; Score 855; DB 4; Length 235;
72.6%; Pred. No. 2.4e-68;
Live 17; Mismatches 44; Indels
                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMUNICATION INFORMATION:
TELECHONE: 650-855-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 72.68 Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTUT13
CLONE: 3116314
CA
USA
                                               94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-049-672A-12
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    STATÈ:
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Gaps

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82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAMLQQHQGHPPKLLSYRNNNRPSGISERL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 LTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
                                                                                                                                                                                                                                                                                                                                            Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Michael, Nancy M
APPLICANT: Accavitt, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     Ouery Match 65.1%; Score 809; DB 4; Length 23 Best Local Similarity 74.2%; Pred. No. 2.8e-64; Matches 158; Conservative 20; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUNTRY: HOUSEON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: CONCURRENTLY Herewith
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 LTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION WOMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-751-359-22
; Sequence 22, Application US/08751359
Patent No. 6143559
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: 512/418-3000
TELERAX: 512/418-3000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 aminotives
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-152-060-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVWAFGGGTKLIVLGQPKAAPSVTLFP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFP 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 LTQPPSVSKDLRQTATLTCTGNNNNVGDQGAAWLQQHQGHPFKLLSYRNNNRPSGISERL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 LTOPPSVSVSPGOTARITCGGDNSR--NEYVHWYQOKPARAPILVIYDDSDRPSGIPERF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.3%; Score 812; DB 4; Length 235; Best Local Similarity 74.6%; Pred. No. 1.5e-64; Matches 159; Conservative 19; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-182-060-88

Sequence 88, Application US/09152060

Sequence 88, Application US/09152060

GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REPRENCE: PZ003P1.US

CURRENT APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER PILING DATE: 1998-03-12

EARLIER PILING DATE: 1998-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-03-14

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                  EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-06-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/048,306
EARLIER APPLICATION NUMBER: 60/048,306
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PACENTIN DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 70
LENGTH: 235
I TYPE: PRI TOME SADIENS
US-09-152-060-70
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EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
   FILING DATE: 1997-03-14
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121 TLTVLGQPKVAPTITLFPPSKEELNBATKATLVCLINDFYPSPVTVDWVIDGS-TRSG-E 178
                                                                                                                                      124 RVTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT 185
4 APLILLAVLAHTSGSLVQAALTQPSSVSANPGETVKITCSGDRS---YYGWYQQKAPGSAP 60
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                                            64 ILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGT
                                                                                                                                                                                                                                                              179 TTAPQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNGTSITKTLKRSEC 229
                                                                                                                                                                                                                                   183 TITPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTEC 233
                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-761-277A-51
Sequence 51, Application US/08761277A
Sequence 51, Application US/08761277A
Septence 51, Application US/08761277A
SENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPADING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION UMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.6%; Score 567; DB 2; Best Local Similarity 100.0%; Pred. No. 2.9e-43; Matches 109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California COUNTRY: United States Of America ZIF: 94104 COMPUTER READABLE FORM: MBDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPE-02406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 100-CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Medlen & Carroll, LLP STREET: 220 Montgomery Street, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MacKnight, Kamrin T. REGISTRATION NUMBER: 38,23
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amino acid
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                                                                                                                                                                                                      64 ILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGT 123
                                                                                                                                                                                                                                                                                                   124 RVTVLGQPKAAPSVTLFPPSSEEL-QANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
                                                                    Gaps
                                                                                                                                                       4 APLILAVLAHTSGSLVQAALTOPSSVSANPGETVKITCSGDRS---YYGWYQQKAPGSAP 60
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                                                                                                           5 AQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQK-PARAP 63
                                                                  7;
                      Length 229;
                                                                                                                                                                                                                                                                                                                                                                                             183 TITPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTEC 233
                                                                                                                                                                                                                                                                                                                                                                                                                           179 TTAPQRQSNSQYMASSYLSLSASDWSSHETYTCRVTHNGTSITKTLKRSEC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                  Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 658.5; DB 4;
; Pred. No. 5.8e-51;
32; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 53.0%; Score 658.5; DB 4; Best Local Similarity 57.6%; Pred. No. 5.8e-51; Matches 133; Conservative 32; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 4433
CITY: Houston
STREET: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,359
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08907146
Patent No. 6316600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Highlander, Steven L
REGISTRATION UNDRER: 37,642
REFERENCE/DOCKET UNDRER: ARSB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/418-3000
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                   53.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 229 amino acids TYPE: amino acid
                                            Best Local Similarity 57.6%
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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US-08-907-146-22
                                         Similarity
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US-08-907-146-22
                   Query Match
Best Local (
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45.1%; Score 560.5; DB 6; Length 200;
Best Local Similarity 53.3%; Pred. No. 2.4e-42;
Matches 112; Conservative 28; Mismatches 51; Indels 19;
;Patent No. 5189147;
APPLICATI: SAITO, HARUO;KRANZ, DAVID M.;ELSEN, HERMAN N.;
;TONEGRAMA, SUSUMU
IITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR
                                                                                            ANTIBODY

MUMBER OF SEQUENCES: 21

CURRENT APPLICATION DATA:

PELLING DATE: 14-NOV-1988

FILING DATE: 14-NOV-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 666,988

FILING DATE: 31-OCT-1984

APPLICATION NUMBER: 620,122

FILING DATE: 13-JUN-1984

SEQ ID NO:10:

LENGTH: 200
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4 ;

80 RFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTL 139 

24 LIQPPSVSVSPGQTARIIC---GGDNSRNEYVHWYQQKPARAPIL-VIYDDSDRPSGIPE 79

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200 LSLTPEOWKSHRSYSCOVTHEGSTVEKTVA 229

Search completed: March 29, 2003, 09:17:39 Job time : 10.3142 secs

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WPI; 1997-108638/10.
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Macaque primatized
Protein sequence o
Ant-CD4 monkey-hum
Novel human diagno
Human novel protei
Macaque primatized
Protein sequence o
Human ovarian anti
                                                                                                                                                       March 29, 2003, 09:06:23 ; Search time 24.0673 Seconds (without alignments) 1295.559 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq-embl/AA1982.DAT:*
| SIDS2/gcgdata/geneseq-embl/AA1982.DAT:*
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| SIDS2/gcgdata/geneseq-geneseq-embl/AA1991.DAT:*
| SIDS2/gcgdata/geneseq-geneseq-embl/AA1991.DAT:*
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1 MRVPAQLLGLLLLWLPGARC......CQVTHEGSTVEKTVAPTECS 234
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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470 segs, 133250620 residues
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                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW01817
AAW13760
AAW11538
AAW14924
ABG19295
ABG19299
AAW14412
AAW1412
AAW1412
AAW1412
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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ant dir	VDUC regions of hu Human secreted pro Human EST encoded Novel human diagno Human bone marrow Anti-HIV-1 recombi Novel human diagno Human immune syste Monoclonal antibod Antibody H84Cs lig	Novel human diagno Novel human diagno Human immune syste Variable and first Novel human diagno Human type antihum Novel human diagno Novel human diagno Human type antihum	dy D polyp type hesus immun d scF
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## ALIGNMENTS

RESULT 1 AAW01817 XX XX AAW01817; AAW01817; XX DT 25-MAY-1997 (first entry) XX XX DF Primatised anti-human B7.1 antigen XX XX XX XX MONOCIONAL antibody; Cynomolgus mon XW MOTIMATISE antibody; B7 antigen; CD XW AUCDIMMUNE disease; idiopathic thro XV XV XV XV Chimeric Howe erythematosus; rheum XX XX Chimeric Macaca cynomolgus; OS Chimeric Homo sapiens. XX XX XX XX XX XX XX XX XX XX XX XX XX	T.1 AAW01817 standard; Protein; 234 AA. AAW01817 standard; Protein; 234 AA. AAW01817, 25-MAY-1997 (first entry) Primatised anti-human B7.1 antigen antibody 7C10 light chain. Monoclonal antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease, idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type I diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma. Chimeric Maccae cynomolgus; Chimeric Homo sapiens.  19-DEC-1996. 06-JUN-1996; 96WO-US10053. (IDEC-) IDEC PHARM CORP. Anderson DR, Brams P, Hanna N. Shestowsky WS.
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WO200189567-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes (see also AAT62509 and AAT62510) are inserted into an expression vector (pref. NBOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                              61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                                                                                                                                                                                                                                                                                                                               GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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                                                                                                                                                                                                                                                                                                                                                               RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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                                                                                                                                                                                                                                                                                                                            1 MRVPAQLIGILILIAMIPGARCAYELTQPPSVSVSPGQTARITICGGDNSRNEYVHWYQQXPA 60
                                                                                                                                                                                                                                                                                                              1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
                      monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VETTTPSKQSNNKYAAASYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                            100.0%; Score 1243; DB 18; Length 234; 100.0%; Pred. No. 1e-70; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaque primatized 7C10 light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW63760 standard; Protein; 234 AA
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                                                            Claim 6; Fig 8A; 81pp; English.
                                                                                                                                                                                                              and graft-versus-host disease.
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Best Local Similarity 100.
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca fascicularis.
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                                                                                                                                                                                                                                       234 AA;
N-PSDB; AAT62509.
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This sequence represents a primatized form of the antibody 7C10 light chain from macaque. This sequence is used in a method which studies new monotonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to monotonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to CC B7.2 (CD86) antibodies and inhibits binding of these antigens to CD28. Such MAD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autofimmune diseases, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, conflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD so nbe conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and production and multigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                           New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
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                                                                                                                                                                                                                  cells, e.g. graft rejection or tumours
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                                                                                                                                                                                                                                                                                                  Example 7; Fig 3a; 87pp; English.
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Chimeric - Macaca sp.
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N-PSDB; AAV35484
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. Crohn's chinitis and eczema, and other types of allergies. The present protein sequence represents the light chain of 7010, a primatised antibody interleukin-2 (IL-2).
                                                                                                                                                                                                                                                                                       Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Fig 3a; 89pp; English.
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                                                                                                                                                                                          Brams
                                                                22-MAY-2001; 2001WO-US16364.
                                                                                                       22-MAY-2000; 2000US-0576424
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Matches 234; Conservative
                                                                                                                                             (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                      Anderson DR, Hanna N,
                                                                                                                                                                                                                               WPI; 2002-089895/12.
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                       29-NOV-2001.
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                                                                1 MRVPAQLLGLLLLMLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA
                                                1 MRVPAQLIGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA
                                                                                                                181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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RESULT 4
AAW14924
ID AAW14924 standard; Protein; 233 AA.
XX
AC AAW14924;
XX
XX
DT 18-OCT-1997 (first entry)
XX
XX
DE Ant-CD4 monkey-human chimeric antibody CE9.1.
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ABG19295 standard; Protein; 247 AA.

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A polypeptide (AAW14924) comprises the lambda variable and constant domains of anti-human CD4 monkey/human chineric antibody CE9.1.

This antibody contains the antigen binding domains (see also AAW14922-23) of a cynomolgue monkey anti-CD4 monoclonal antibody, a human heavy chain constant region of gamma 1 isotype and Gmla, Gmlz allotype, and a human lambda light constant region of the Oz minus, cog minus genotype, and a human lambda light constant region of the Oz minus, cog minus genotype, were cloned into mammalian expression vector TCAE 6, and chimeric antibody was produced in CHO cells. CE9.1 binds to domain 1 of human, but not macaque, CD4, a region involved in the interaction with MHC class II molecules on antigenpresenting cells. It shows potent immunomedulatory activity with low immunogenicity in humans, and can be used to treat autoimmune constants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                  CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgue monkey; autolmmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LLGLLAHFTDSA-ASYELSQPRSVSVSPGQTAGFTCGGDNVGRKSVQWYQQKPQQAPVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT
                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, esp. useful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.7%; Score 1015.5; DB 18; Length 233; Best Local Similarity 86.0%; Pred. No. 1.8e-56; Matches 196; Conservative 10; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 79-80; 155pp; English
                                                                                                                                                                                                                                                                                                                                       Hanna N, Newman RA, Reff ME;
                                                                                                        Chimaeric Macaca cynomolgus;
                                                                                                                                                                                                                                   96WO-US14324
                                                                                                                                                                                                                                                                  95US-0523894
                                                                                                                                                                                                                                                                                                      (IDEC-) IDEC PHARM CORP.
                                                                                                                     Chimaeric Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-201913/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA;
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT62867
                                                                                                                                                                                                                               05-SEP-1996;
                                                                                                                                                                                                                                                                06-SEP-1995;
                                                                                                                                                          WO9709351-A1
                                                                                                                                                                                             13-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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ABG19295
δ
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ABG19295;

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polypeptide (II) sequences (I) brimers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The characters are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in disponsities, forenise, generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and much on ediagnostic amino acid sequences ABG00010-ABG30377 represent novel human condisponsible for generic disorders of the invention.

Note: The sequence data for this patent did not appear in the printed and the fire into into into a condition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 PILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LGLLLLWLPGARC----AYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||
|-----SHCTASVTSFVLAQPPSVSVAPGETARITCGADNIGRRSVHWYQQRPGQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%; Score 991.5; DB 2
81.9%; Pred. No. 6.3e-55;
live 14; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 49654; 103pp; English.
                                                                             Novel human diagnostic protein #19286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                     10-MAR-2001; 2001WO-US08631.
                                    18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS83482
                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biodiversity
                                                                                                                                                                                                                                                               11-OCT-2001.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome condymerase chain reaction (PCR) primers, oligomers, and for chromosome condymerase chain reaction of (II). The polymcleotides are also used in diagnostics as expressed sequence tags for reformer normal activity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving contribution and propertied in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating of isolayeristes and polymchecides sequences have applications in disponsitive for generation sequences have applications in disponsitive for generation dental and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human condition, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                 196 TTTPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.8%; Score 979; DB 22; Length 238; Best Local Similarity 80.3%; Pred. No. 3.7e-54; Matches 187; Conservative 13; Mismatches 21; Indels 15
TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 49658; 103pp; English.
                                                                                                                                                                                                                                            Novel human diagnostic protein #19290.
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                                                                                                                               ABG19299 standard; Protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                      (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS83486
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
                                                                                                                                                                                                      18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2001.
                                                                                                                                                                  ABG19299;
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183
                                                                                                             ABG19299
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12 LLWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61

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The invention relates to polynucleotides encoding novel human probability of proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as method of protein expression or activity. The polypeptides can be used as method of protein expression or activity. The polypeptides can be used as probes and polypeptides are used to identify compounds which bind to the polypeptides. Polyucleotides of the invention are used as probes and production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem call disorders, vegenerating bone, cartilage, tendon, ilgament and/or nerve tissue, wound healing, treating burns, promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; octostatic; neuroprotective; vulnerary; noctropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder;
                                                                                                                  125
                                                                                                                                                                                                         185
                                                                 62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
                                                                                                                                                         122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage
68 SPVLVIFQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWD--SSTAVFGG
                                                                                                                                                                                                    126 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV
                                                                                                                                                                                                                                                   182 ETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                             186 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 805-806; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              AAU14412 standard; Protein; 232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human novel protein #283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-451939/48.
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AAU14412
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the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host diseases, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 179
                                                                                                                                                                                                                                                                                                                                                                         61 SPVLVIYQDDKRPSEIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWD-SSTAVMFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                         122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                                                                                                                                                                                                                                                                                                                                                    62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
                                                                                                                                                                                                                                         11; Gaps
                                                                                                                                                                                                                                                                                                   12 LLWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 ETTTPSKOSNNKYAASSYLSLTPEOWKSHRSYSCQVTHEGSTVEKTVAPTECS 232
                                                                                                                                                                                                       DB 22; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 ETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                         21; Indels
                                                                                                                                                                                                   78.6%; Score 976.5; DB 2;
80.3%; Pred. No. 5.1e-54;
ltive 14; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaque primatized 16C10 light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanna N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US19906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0746361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-1998 (first entry)
                                                                                                                                                                                                                                         Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IDEC-) IDEC PHARM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-286601/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca fascicularis.
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                      232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV35488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9819706-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1998.
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW63764;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW6376,
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This sequence represents a primatized form of the antibody 16C10 light

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chain from macaque. This sequence is used in a method which studies new monotonal antibodies (MAD' 8) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibite binding of these antigens to CD28. Such MAD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic ansemia, nost diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagente. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and inhibits antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRVPAQLIGLLILWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

78.3%; Score 973; DB 19; Length 236;
Best Local Similarity 80.1%; Pred. No. 8.6e-54;
Matches 189; Conservative 13; Mismatches 32; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA;
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121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
  119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                                                         179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                     181 AGVETTTPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                            AAU11645 standard; Protein; 236 AA
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Protein sequence of primatised form of the light chain of 16C10 antibody.
                                                                                                          Human, macaque monkey, light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B Cell cancer; metastasis; tumour; B Cell lymphoma; B Cell lowkaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                         interleukin-2; IL-2; mutant; mutein.
                                                             (first entry)
                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                Chimeric - Homo sapie
Chimeric - Macaca sp.
                                                             12-MAR-2002
                                    AAU11645;
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22-MAY-2001; 2001WO-US16364.
                                                                                                                                              22-MAY-2000; 2000US-0576424
                                                                                                                                                                                (IDEC-) IDEC PHARM CORP.
                                  WO200189567-A1.
                                                                      29-NOV-2001.
Synthetic.
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Brams P;

Hanna N,

Anderson DR,

Human, ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; cardiovascular disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;

Human ovarian antigen HCNSF57, SEQ ID NO:2493.

22-AUG-2002 (first entry)

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which specifically binds to Br. 1 antigen (CDB0) and/or Br. 2 antigen (CDB6) for inducing the apoptosis of Br+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, and cancer where B cells promote the growth and/or metastasis of tumours, idiopathic thrombocytopenia purpura, systematic lupus, erythematosus, type I diabetes mellitus, rheumatoria strictis, psoriasis, aplantic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistence to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, integtinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present protein sequence represents the light chain of 16ClO, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                       CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
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                                                                                  Use of monoclonal antibody which specifically binds to B7.1 antigen
                                                                                                                                                                                                                                           present invention relates to a new use of a monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRVPAQLIGILILMIPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.3%; Score 973; DB 23; Length 236; Best Local Similarity 80.1%; Pred. No. 8.6e-54; Matches 189; Conservative 13; Mismatches 32; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP41361 standard; Protein; 269 AA.
                                                                                                                                                                                              Example 8; Fig 5a; 89pp; English.
                  WPI; 2002-089895/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-2 (IL-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AA;
                                        N-PSDB; AAS17246.
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ABP41361
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ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
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                             182
                                                                                                                                            RESULT 11
                                                                                                                                                                    AAW01823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also concentrated by identical and polypuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens and the use of ovarian antigens, and the use of ovarian antigens in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system clisorders (e.g., infertility, disorders of pregnancy, anovulation, and infertility, disorders of pregnancy, anovulation, clisorders (e.g., infertility, disorders of pregnancy, anovulation, and isorders disorders, infertility, disorders of pregnancy, anovulation, clisorders, infertility, disorders of pregnancy, anovulation, another disorders, infertility, disorders of e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., cliamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., cancentia, systemic lapsorders, neurological disorders, gastrointestinal disorders and uninary system disorders. Ovarian antigen polypeptides and compute ovarian antigen expression or activity. The polymucleotides may also be used in screening for compounds which clientication of individuals and in screening for compounds which in disease disagnosis, drug targeting and phenotyping. The printed cequence represents a human ovarian antigen of the invention. Sequence expresents a human ovarian antigen of the invention.

Specification, but was obtained antigen of the invention of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTRVTVLGQPKAAPSVTLPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 GTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 LLWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.3%; Score 973; DB 23; 79.8%; Pred. No. 9.8e-54; tive 14; Mismatches 21;
antiiñflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID No 2493; 2922pp; English.
                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                          07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                                      07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-147878/19.
N-PSDB; ABQ54438.
                                                                                                                                                                                                                                                                                                                                      Birse CE, Rosen CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AA;
                                                                                               WO200200677-A1
                                                      Homo sapiens.
                                                                                                                                              03-JAN-2002
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2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human bB7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                             Primatised anti-human B7.1 antigen antibody 16C10 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 236;
217 ETTTPSKQSNNKYAASSYLSLTPEQWKSHXSYSCQVTHEGSTVEKTVAPTECS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shestowsky WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.3e-53
14; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Fig 10A; 81pp; English.
                                                                                                                                                                                                   AAW01821 standard; Protein; 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0487550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson DR, Brams P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-108638/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT62512
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method off treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides can be used as molecular weight markers, for dentify compounds which bind to the polypeptides. Polypucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to target antibodies/ellcit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, and perfernent arroke, immune deficiency expenditing from harrerial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sclerquis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, atthmeshersene, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                  immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                               181 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                     Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 553; 894pp; English.
                                                                                                                                                        AAU14176 standard; Protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001; 2001WO-US02623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                     Human novel protein #47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-451939/48.
N-PSDB; AAS22481.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200155437-A2
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                      24-OCT-2001
                                                                                                                                                                                        AAU14176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rang YT,
                                             179
                                                                                                                          RESULT 12
AAU14176
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                                                                                                                                                                                                                                                                                                                                                                                     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                      9
                                                                                                                              Gaps
                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                       61 SPVLVIYRHSKRPSGIPERFSGSNSGNTATLTISGTQVMDEADYYCQAWD--SSIVVFGG
                                                                                                                                                                                          12 LLWLP-----GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR
                                                                                                                                                                                                                                                   1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYASWYQQKAGQ
                                                                                                                                                                                                                                                                                                                     62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                           Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 ETTTPSKOSNNKYAASSYLSLTPEOWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                           23; Indels
                                                           DB 22;
                                                        77.2%; Score 959; DB 22, 79.0%; Pred. No. 6.4e-53
                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 53443; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #23075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG23084 standard; Protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                       Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73
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                                                                                         Best Local Similarity
231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
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Sequence
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                                                           Query Match
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disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at tp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 SPLLVLYQDTNRPSGIPERFSGSNSGNTATLTISETQAMDEGDYYCQAMD--SNTVVFGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGQTASITCFGDKLGDKYSSWYQQKPGQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTKLTVLSQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.2%; Score 959; DB 22; Length 234; 78.5%; Pred. No. 6.5e-53; ive 17; Mismatches 21; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 582; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU14236 standard; Protein; 232 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 78.35
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel protein #107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-451939/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           234 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
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The invention relates to polynucleotides encoding novel human cative domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, response, to determine quantitative corrects are cell disorders, response, to determine quantitative disorders, requererating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, contraceptive, treating osteoporosis and osteoarthritis, anaemia, allored, surcke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, contraceptive, treating osteoporosis and osteoarthritis, and infection.

The profile infection or from autoimmunity, cancer, allergy, asthma, contraceptive, from autoimmunity, cancer, allergy, and infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
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; Pred. No. 6.9e-53;
16; Mismatches 23
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/label= FR1
/note= "Framework region"
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78.5%;
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'note= "Wild-type Ser-Tyr-Glu substituted by
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/label= CDR1
/note= "Complementarity determining region"
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/label= CDR3
/note= "Complementarity determining region"
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                                                                                                             note= "Wild-type Arg substituted by Thr"
                                                                           'note= "Wild-type Met substituted by Thr"
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/label= FR3
/note= "Framework region"
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/label= CDR2
                                      Gln-Ser-Val"
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/label= FR2
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23-FEB-2001; 2001WO-US05973

23-FEB-2000; 2000US-0511139 22-FEB-2001; 2001US-0791153

(AMGE-) AMGEN INC.

Sullivan JK; Boyle WJ, Deshpande RV, Hitz A,

WPI; 2001-557706/62. N-PSDB; AAS13364.

Antibodies that bind antagonistically to osteoprotegrin binding protein, useful for treating osteoporosis, metastasis of cancer to bone, rheumatoid arthritis, hypercalcaemia of malignancy and steroid-induced osteoporosis

Claim 10; Fig 8; 239pp; English.

The invention relates to an antibody or antigen binding domain (or fragment, variant or derivative), which binds to an osteoprotegrin binding protein (OPGDP) and which is an antagonistic antibody.

The antibody or antigen binding domain may be administered to inhibit osteoclast formation or activation, inhibit bone resorption in a mammal, prevent or treat loss of bone mass in a mammal and to prevent or treat tumour cell growth in bone. The loss of bone mass results from osteoporosis, metastasis of cancer to bone, rheumatoid arthritis, hypercalcaemia of malignancy and steroid-induced osteoporosis. The present sequence is a full length, cloned anti-OPGDp antibody light

Ä \$18 Sequence

ö 84 SKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFPPS 143 SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLT 187 SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLT 203 Gaps LTOPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERFSG ö Length 218; Indels 19: DB 22; 75.9%; Score 944; DB 22; 84.4%; Pred. No. 5.2e-52; iive 14; Mismatches 15 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 218 PEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234 Matches 178; Conservative Best Local Similarity Query Match 24 œ 68 144 128 204 ò g ò d ò

Search completed: March 29, 2003, 09:10:14 Job time : 26.0673 secs

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    Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 1424, Ap
Sequence 202, Appl
Sequence 38, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 88, Appl
Sequence 88, Appl
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RESULT 1

US-10-124-905-2

is Sequence 2. Application US/10124905

patent No. US20020166136A1

if PAPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONEY WONCLOUNL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "MONEY WONCLOUNL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PHARM-CEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: INMOSUPRESANTS"

TOTHE OF INVENTION: PHARM-CEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: INMOSUPRESANTS"

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Matches 189; Conservative
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "PARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
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                                                                                                                                                                                                                                                                                                             61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                                                                                                                                                                                                                                                                                                          121 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
                                                                                                                                                                                                                                                                                 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                                                                                                                                                                                                                                                                                    GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
                                                                                                                                                      Gaps
                                                                                                                                                                                                1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
                                                                                                                                                                                                                                   1 MRVPAQLIGLILMIPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                      ;
0
                                                                                                             Length 234;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                           100.0%; Score 1243; DB 9;
100.0%; Pred. No. 3.8e-56;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         012712-131
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,556
FILING DATE: 07-UTN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09948429B Patent No. US20020177689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                        Query Match
Best Local Similarity 100.
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 234 amino acids
TYPE: amino acid
TOPON/GY: linear
                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-09-948-429B-2
        amino acid
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APPLICANT: Anders
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Anderson, Darrell R.
VERTICN: "MONNEX MONOCLONAL ANTIBODIES SPECIFIC
VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
VENTION: IMMUNOSUPPRESANTS"
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                                                                                                                                                                                                                                                                                                                                                   GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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                                                            Gaps
                                                                                                                                                       1 MRVPAQLIGILILMLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
                                                                                                                   1 MRVPAQLLGLLLUWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHSYSCQVTHEGSTVEKTVAPTECS 234
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   Length 234;
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                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: RIADABLE FORM:
MEDIUM TYPE: RIADABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
FILING DATE:
CLASSIFICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
Score 1243; DB 9;
Pred. No. 3.8e-56;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBOD
TITLE OF INVENTION: TO HUMAN B7.2
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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Patent No. US20020166136A1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6220
TELEFAX: 703-836-2221
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
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) LOCATION: (221)
) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
              61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                    119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDPYPGAVTVAWKADSSPVK 178
                                                                                         121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRASDHPVFGGGTRVTVLGQPKAAPSVTLFPPSSEBLQANKATLVCLISDFYPGAVTVAW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 YVHWYQQKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVW 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RVPAQLLG-LLLLWLP-----GARCAYELTQPPSVSVSPGQTARITCGGDNSRNE 50
                                                                                                                                                   179 AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.3%; Score 936.5; DB 10; Length 244; 75.4%; Pred. No. 9.2e-41; ive 15; Mismatches 34; Indels 11;
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFRENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR PLILING DATE: 2000-03-08
PRIOR FILING DATE: 10999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1424
                                                                                                                                                                                                                                                               ; Sequence 1424, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.4%
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (59)
OTHER INFORMATION: X
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US-09-925-301-1424
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US-09-747-669-6
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TITLE OF INVENTION: TO HUMAN 17.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMANCEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                          PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPV 118
                                                                                  FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                                                                                                             PARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADXYCQVWDRASDHPV 118
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                                                                                                                                                                                                                                    AGVETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.3%; Score 973; DB 9;
80.1%; Pred. No. 1.3e-42;
tive 13; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UTN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPRENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-948-429B-10
; Sequence 10, Application US/09948429B
; Patent No. US20020177689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.1%
Matches 189; Conservative
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
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APPLICANT: Anders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
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Sequence 38, Application US/09974449

Sequence 38, Application US/09974449

Sequence 38, Application US/09974449

GENERAL INFORMATION:

APPLICANT: Kricek, Franz

APPLICANT: Kricek, Franz

APPLICANT: Kricek, Franz

APPLICANT: Wogel, Monique

TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST

TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST

TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST

TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR

FILE REFERENCE: 4-30888A

CURRENT APPLICATION NUMBER: US/09/974,449

CURRENT FILING DATE: 2001-10-10

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38

LENGTH: 219

TENDER: DEAD
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73
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                                                                                              134 APSVTLFPPSSEELQANKATLVCLLSDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK
----QVWDRASDHPVFGGGTRVTVLGQPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 219;
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                                                                                                                                                                                                      194 YAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                69.6%; Score 865.5; DB 10; 78.7%; Pred. No. 3.1e-37; tive 16; Mismatches 25;
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CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR PILING DATE: 1998-09-11
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     80 RFSGSKSGNTATLTINGVEAGDEADYYC-
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; Sequence 70, Application US/09852797
; Patent No. US20020172994Al
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-09-974-449-38
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Publication No. US20020183500A1

GRNERAL INFORMATION:
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT APPLICATION NUMBER: 60/252,054
PRIOR PILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
          APPLICANT: Saieh, Mansoor
TITLE OF INVENTION: ANTIGEN BINDING FRACMENTS, DESIGNATED
TITLE OF INVENTION: ANTIGEN BINDING FRACMENTS, DESIGNATED
TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
TITLE OF INVENTION: AND DETECTION OF CANCERS
TITLE OF INVENTION: AND DETECTION OF CANCERS
TITLE OF INVENTION: AND DETECTION OF CANCERS
TITLE OF INVENTION: AND DETECTION OF CANCERS
CURRENT APPLICATION UNMBRR: US/09/747,669
CURRENT FILING DATE: 2002-04-08
PRIOR FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 235
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 VIVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.3%; Score 873.5; DB 9; Length 221; Best Local Similarity 76.9%; Pred. No. 1.2e-37; Matches 170; Conservative 16; Mismatches 18; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 LTQPPSVSVSPGQTARITCGGDNSR----NEYVHWYQQKPARAPILVIYDDSDRPSGIPE 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic construct
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SOFTWARE: Patentin version 3.1
SEQ ID NO 202
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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US-10-001-857-202
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83 SASRSGATSSLTITGLQPEDEADYYCAAYDSSLAVMMFGGGTKLTVLGQPKAAPSVTLFP 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS
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Best Local Similarity 74.6%; Pred. No. 1.6e-34;
Matches 159; Conservative 19; Mismatches 33;
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Sequence 70, Application US/09652659A

PAPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFRENCE: PZ00310200165-19

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: 60/04656

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR FILING DATE: 1990-03-12

PRIOR PRIOR PLING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR PRIOR PLING DATE: 1997-03-14

PRIOR PLING DATE: 1997-03-14

PRIOR PLING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

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PRIOR PRIOR FILING DATE: 1997-05-30
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     PRIOR APPLICATION NUMBER: 60/048,35/
PRIOR FILING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 60/048,70
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PACENTIN VEY: 2.0
SEQ ID NO 70
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.3%; Score 812; DB 9; Length 235; 74.6%; Pred. No. 1.6e-34; Live 19; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 70, Application US/09853161
Fatent No. US20020076756A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
FRIOR PILING DATE: 2001-02-02
FRIOR APPLICATION NUMBER: 09/152,060
FRIOR PELING DATE: 1998-09-11
FRIOR FILING DATE: 1998-03-12
FRIOR FILING DATE: 1998-03-14
FRIOR APPLICATION NUMBER: 60/040,762
FRIOR PILING DATE: 1997-03-14
FRIOR APPLICATION NUMBER: 60/040,762
FRIOR FILING DATE: 1997-03-14
FRIOR FILING DATE: 1997-03-14
FRIOR FILING DATE: 1997-05-30
FRIOR FILING DATE: 1997-05-30
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        APPLICATION NUMBER: PCT/US98/04858
PRIOR APPLICATION NUMBER: PCT/US98/0485
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR PLING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-05
PRIOR PELING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ 1D NOS: 118
NUMBER OF SEQ 1D NOS: 118
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US-09-852-797-70
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Best Local Similarity
Matches 159; Conserv
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US-09-853-161-70
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LENGTH: 235
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                                                                                               23 LTQPPSVSKDLRQTATLLTCTGNNNNVGDQGAAWLQQHQGHPFKLLSYRNNNRPSGISERL 82
2; Gaps
                                                         24 LIQPPSVSVSPGQTARITCGGDNSR--NEYVHWYQQKPARAPILVIYDDSDRPSGIPERF 81
                                                                                                                                                                                                                                                                                                                               PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKOSNNKYAASSYLS
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33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 88, Application US/09853161
Patent No. US20020076756A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFRENCE: P2003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR PILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-12
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR PILING DATE: 1997-03-14
PRIOR PELICATION NUMBER: 60/040,70
PRIOR PELICATION NUMBER: 60/040,70
PRIOR PILING DATE: 1997-03-04
PRIOR PILING DATE: 1997-03-06
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR PELING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,369
PRIOR APPLICATION NUMBER: 60/048,369
PRIOR APPLICATION NUMBER: 60/048,369
PRIOR APPLICATION NUMBER: 60/048,369
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
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   Matches 158; Conservative 20; Mismatches
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Best Local Similarity 74.2%,
Matches 158; Conservative
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US-09-853-161-88
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                                                                                                                                                                                                                                                                  Query Match 65.3%; Score 812; DB 10; Length 235; Best Local Similarity 74.6%; Pred. No. 1.6e-34; Matches 159; Conservative 19; Mismatches 33; Indels
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE SPEERENCE: P2003P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT APPLICATION NUMBER: 09/265,583
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-14
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
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PRIOR FILING DATE: 1997-05-30
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PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 88
LENGTH: 235
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Patent No. US20020172994A1
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   , NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 235
LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-852-797-88
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Best Local Similarity
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142 PSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLS 201
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                                          143 PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKOSNNKYAASSYLS 202
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Best Local Similarity 74.2%; Pred. No. 2.2e-34;
Matches 158; Conservative 20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                         Sequence 88, Application US/09852659A
Patent No. US20020077287A1
GENERAL INFORMATION:
APPLICATI: ROBER et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P4
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CURRENT PELLING DATE: 2001-05-11

PRIOR PELLING DATE: 2001-05-11

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PRIOR PILLING DATE: 2001-02-02

PRIOR FILLING DATE: 1998-09-11

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ORGANISM: Homo sapiens
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140 FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSY 199
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                                                            APPLICANT: Waldmann, Herman
APPLICANT: Waldmann, Mark
TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
FILE REPERENCE: Waldmann
CURRENT APPLICATION NUMBER: US/09/736,371B
CURRENT APPLICATION NUMBER: 9015-905
PRIOR APPLICATION NUMBER: 9015-905
PRIOR APPLICATION NUMBER: 9015-907-21
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PARENTIN OFF: 2.1
SOFTWARE: PARENTIN OFF: 2.1
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Sequence 19, Application US/09736371B Patent No. US20020131968A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Rattus
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Search completed: March 29, 2003, 09:38:36 Job time : 10.9705 secs

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Copyright (c) 1993 - 2003 Compugen_Ltd.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
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Last annotation update)
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ALIGNMENTS
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-!- MISCELLANBOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE POUND IN PROTEIN PROTEIN PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN HAS THE KERN+ MARKER, AND THE MCG+ MARKER.

-!- MISCELLANBOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE 3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-1) & THE KERN-/OZ+ SEQUENCE (LAMBDA-1) & THE KERN-/OZ+
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EMBL; L38562; AAB6581.1; ALT INIT.
EMBL; X51754; CAB38569.1; ALT_INIT.
EMBL; X51755; CAA36049.1; -.
EMBL; X51755; CAA36051.1; -.
PIR, A02125; L2HU.
PDB; ZMCG; 15-JUL-92.
PDB; 7FAB; 31-JAN-94.
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InterPro; IPR003597; Ig_c1.
Pfan; PF00047; Ig, 1.
SWART; SW00407; IGc1; 1.
PROSITE; PS00290; IGc1/HC; 1.
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Genew, HGNC:5856; IGLC2.
Genew, HGNC:5857; IGLC3.
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01-APR-1990 (Rel. 14, Last sequence update)
115-UTN-2002 (Rel. 41, Last annotation update)
Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-
related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
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Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
McKearn J.P.;
"Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
expressed in pre-B cells and may encode the human immunoglobulin
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
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DISÜLFID 27 86 INTERCHAIN (WITH HEAVY CHAIN).
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/FIId=VAR 003898.
S -> T (IN MCG+ MARKER).
/FIId=VAR 003899.
S -> G (IN KERN+ MARKER).
/FIId=VAR 003900.
T -> K (IN MCG+ MARKER).
/FIId=VAR 003901.
R -> K (IN OZ+ MARKER).
/FIId=VAR 003902.
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Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989).
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44.1%; Score 548; DB 1;
Best Local Similarity 100.0%; Pred. No. 9.6e-38;
Matches 105; Conservative 0; Mismatches 0;
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Homo sapiens (Human).
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111 AA;
        NCBI_TaxID=9606;
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J REGION (BY SIMILARITY TO LAMBDA
LIGHT-CHAIN).
C REGION (BY SIMILARITY TO LAMBDA
LIGHT-CHAIN).
; 9133A7742B943C79 CRC64;
                                      Evans R.J., Hollis G.F., "Genomic structure of the human Ig lambda 1 gene suggests that it may be expressed as an Ig lambda 14.1-like protein or as a canonical B cell Ig lambda light chain: implications for Ig lambda gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 WPRGFQSKHNSVTHVFGSGTQLTVLSQPKATPSVTLFPPSSEELQANKATLVCLMNDFYP 142
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                                                                                                                                      U. EXP. Med. 173:305-311(1991).

-1- SUBUNIT: Associates non-covalently with VPREBI.

-1- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

-1- DATABASE: NAME-PROW; NOTE-PROW 1:64-67(2000);

WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/696419174_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LV3B HUMAN STANDARD; PRT; 111 AA.
B0748; 180748; 180748; 180748; 15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. V-III region LOI.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promise Pro0047; 1g; 1. SMART; SM00407; 1G:1; 1. PROSITE; PS00290; IGCMHC; 1. Immunoglobulin domain; B-cell; Signal SIGNAL
                    MEDLINE=91108327; PubMed=1703205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M27749; AAA36100.1; -.
EMBL; M34513; AAA36096.1; -.
EMBL; M34511; AAA36096.1; -.
EMBL; M34512; AAA36096.1; JOINED.
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InterPro, IPR003597, Ig_cl.
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HSSP; P01842; 7FAB.
Genew; HGNC:5870; IGLL1.
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OC EUKARY
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RARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BARARA BA
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Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
Jokirantiogenic lambda light chain dimer: a unique human
miniautoantibody agaling complement factor H.";
J. Immunol. 163:4890-4596 (1999).
-!- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
                                                                                                                                                                                                                                                                     -1- SUBBUNIT: HOWODINER.
-1- DISEASE: THE BLOCKING OF FACTOR H BY LOI PROTEIN LEADS TO THE DEVELOPMENTAL OF MEMBRANOPROLIFERATIVE GLOMERULONEPHRITIS (MFGN).
DEVELOPMENTAL OF MEMBRANOPROLIFERATIVE GLOMERULONEPHRITIS (MFGN).
INTERPRO; 12P0016; 1g MHC.
INTERPRO; 1PR003596; 1g V.
Pfam; PR00047; 1g; 1.
SMART; SMO047; 1g; 1.
SMART; SMO0406; 1GV; 1.
SMART; SMO0406; 1GV; 1.
SMART; SMO0406; 1GV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eur. J. Biochem. 50:49-69(1974).
-!- MISCELLANBOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA CHAIN SUBGROUP V.
-!- MISCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.0%; Score 472; DB 1; Length 111; 76.6%; Pred. No. 1.4e-31; Live 14; Mismatches 12; Indels
SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
11935 MW; 69498EBEFDE82053 CRC64;
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HSSP; P80748; 2LOI.
INTERPOO; IPRO03006; Ig_MHC.
INTERPOO; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
SWART; SMO0406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
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SEQUENCE 108 AA; 11342 MW; B8E8ED9C09C9E451
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g lambda chain V-V region DEL.
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MEDLINE=78000254; PubMed=409425;
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PIR; A02129; L1PG.
HSSP; P01847; 2MCG.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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**REDLINE=78187276; PubMed=418804;

**MEDLINE=78187276; PubMed=418804;

**Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;

Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;

**Chain acid sequence of the variable region of the light (lambda)

**Chain from human myeloma cryoimmunoglobulin IgG Hil.";

**Line from human myeloma cryoimmunoglobulin IgG Hil.";

**Line from human myeloma cryoimmunoglobulin IgG Hil.";

**Line from human myeloma cryoimmunoglobulin IgG Hil.";

**Line from human myeloma cryoimmunoglobulin IgG Hil.";

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                                                                                                           Gaps
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1-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 03). Last annotation update)
15-JUL-1999 (Rel. 38). Last annotation update)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                35.7%; Score 444; DB 1; Length 108; 73.1%; Pred. No. 2.4e-29; ive 15; Mismatches 14; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                       Best Local Similarity 73.19
Matches 79; Conservative
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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P01717;
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P01846;
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130 OPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
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Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
-!- MISCELLANEOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (843).
MEDLINE-82220143; PubMed-6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                          immunoglobulin lambda chains.";
Biochemistry 16:3765-3772(1977).
-!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MIXTURE OF NORWAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Somatic variants of murine immunoglobulin lambda light chains.";
Nature 298:380-382(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
Nature 290:65-67(1981)
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MEDLINE=81148806; PubMed=6259534;
Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
Gefter M.L., Baltimore D.;
Novotny J., Franek F., Margolies M.N., Haber E.; "Amino acid sequence of normal (microheterogeneous) porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
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MEDLINE-8014953; PubMed=6812053; Segling E., Miller J., Wilson R., Storb U.; Esolution of mouse immunoglobulin lambda genes."; Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 74.3%; Pred. No. 4.9e-27;
Matches 78; Conservative 9; Mismatches 18.
                                                                                                                                                                                                                                                                                              Pfam; PF00047; igg: 1.
PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
NON TER 1 1 1
DISULPID 27 86
DISULPID 104 104 INTERCHAIN (WITH H
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G lambda-1 chain C region.
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MEDLINE=71107854; PubMed=5276767;
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 NORMÂL LAMBDA-2 CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING
A LARGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
APPEARS COMPLETELY NORMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Backo K., Braun D., Hilschmann N.;
"Pattern of antibody structure, the primary structure of monoclonal immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                33.1%; Score 412; DB 1; Length 105; 71.4%; Pred. No. 8.6e-27; Live 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                              ET -> TE (IN REF. 4).

0 -> E (IN REF. 4).

MISSING (IN REF. 4).

HS -> SH (IN REF. 4).

S -> SS (IN REF. 4).

E -> Q (IN REF. 4).

W, A89F2B09BCFCA018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 SNNKYAASSYLSLTPEOWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SNNKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKSLSRADCS 105
                                                                                                                                              EMBL; J00582; AAA51636.1; -.
EMBL; J00587; AAB59672.1; -.
PIR; AQ126; LIMS.
HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
Pfam; PF0047; ig; 1.
SMO447; ig: 1.
PROSITE; PS00290; IG_MHC; 1.
Imunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).
-1- MISCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.
HSRP, B01981; LAHUBU.
HSRP, B01481; LLOI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Ffam; FF00047; Ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-IV region Bau.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 106 AA.
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104
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11575 MW;
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                                                                                                                                                                                                                                                                                                                                                                                        105 AA;
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P01715;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81122740; PubMed=6780787;
Kojima M., Odani S., Ikenaka T.;
"Anino acid sequence of the lambda type light chain of a human IgGl
myeloma protein (MOT) with unusual antigenicity: a possible new
myeloma protein (MOT) with unusual antigenicity: a possible new
subgroup of lambda chain having a unique N-terminal sequence.";
Mol. Immunol. 17:1407-1414(1980)

-!- MISCELLANEOUS: THIS SEQUENCE REPRESENTS A NEW LAMBDA CHAIN
SUBGROUP. IT HAS AN AMINO-TERMINAL EXTENSION OF THREE RESIDUES
COMPARED WITH OTHER HUMAN LAMBDA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARKERS.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                  Length 106;
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                                                                                             32.7%; Score 407; DB 1; Length 10
71.3%; Pred. No. 2.2e-26;
Live 10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                  82 SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVLG 129
                                                                                                                                                                                                                                                                                                             Query Match 32.2%; Score 400; DB 1; Length 11 Best Local Similarity 69.4%; Pred. No. 8.5e-26; Matches 75; Conservative 10; Mismatches 23; Indels
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Immunoglobulin V region; Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homo sapiens (HumavNI region MOT.
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(Rel. 17, Last sequence update)
(Rel. 38, Last annotation update)
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HSSP; P80748; ZLOI.
INTERPRO; IPRO03006; Ig_MHC.
INTERPRO; IPRO03596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00466; IGV; 1.
Immunoglobulin V region.
NON_TER 111 111
                                                                                          Query Match
Best Local Similarity 71.3*
Matches 77; Conservative
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P01847;
21-JUL-1986 (
01-FEB-1991 (
15-JUL-1999 (
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P01720;
                          NON TER
SEQUENCE
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LV7A_HUMAN
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LAC_RABIT
ID_LAC_R3
AC P0184
DT 21-JU
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DT 15-JU
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SEQUENCE

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Rāttus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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N-LINKED (GLCNAC. . .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holm E., Sletten K., Husby G.;
"Structural studies of a carbohydrate-containing
immunoglobulin-lambda-light-chain amyloid-fibril protein (AL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variable subgroup III. ";
Biochem. J. 239:545-551(1986).
-i- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED HOMOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 106
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67.6%; Pred. No. 1.4e-25;
tive 13; Mismatches 20; Indels
                                                                                                                                                                                                  SGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVTVL 128
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HSSP, P80748; ZLOI.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Amyloid; Glycoprotein.
DISULFID 90 90 N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
11g lambda-1 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-IV region MOL.
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MEDLINE=87305594; PubMed=3114047;
Steen M.L., Hellman L., Pettersson U.;
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MEDLINE=87156515; PubMed=3103603;
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Matches 73; Conservative
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P06889;
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P20766;
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LV4E HUMAN
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Milstein C., Clegg J.B., Jarvis J.M.;
"Immunoglobulin lambda-chains. The complete amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Ig lambda chain C region.
Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                               Garcia I., Jaton J.-C.;
"The primary structure of the constant region of Basilea-rabbit immunoglobulin lambda-chains.";
Biochem. J. 197:177-183(1981).
-!- MISCELLANBOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 104 INTERCHAIN (WITH HEAVY CHAIN).
105 AA; 11484 MW; B427513272E8663D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 72.4%; Pred. No. 9.6e-26;
Les 76; Conservative 9; Mismatches 20; Indels
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HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
Pfam; PF00047; ig; 1.
FMART; SM00407; iGc1; 1.
PROSITE; PS00290; IG MHC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin C region.
NON TER
DISULPID 27 86
DISULPID 104 104
DISULPID 105 AA; 11484 MW; B427513272E8663D CR
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-IV region X.
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Matches 76; Conserv
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RESULT 11 LV4B\_HUMAN

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@lsb-sib.ch).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene."; Gene 55:75-84(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=87305594; PubMed=3114047;
Steen M.L., Hellman L., Pettersson U.;
"The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";
Gene 55:75-84(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.0%; Score 385.5; DB 1; Length 104; 66.7%; Pred. No. 1.2e-24; tive 17; Mismatches 17; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (WITH HEAVY CHAIN)
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104 AA; 11565 MW; CBF71811F4BC878A CRC64;
                                                                                                                                                                                                                                                                                         PFam; PF00047; ig; 1.
SMART; SM00407; IG; 1.
PROSITE; PS00290; IG MHC; 1.
Imunoglobulin domain; Immunoglobulin C region.
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 lambda-2 chain C region.
Rattus norvegicus (Rat)
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                                                                                                                                                                                                          EMBL; M22520; AAA41419.1; ALT_INIT.
PIR; A27390; A27390.
HSSP; P01842; 7FAB.
InterFro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
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PIR; B27390; B27390.
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003597; Ig_cl.
Pfam; PF00047; ig; 1.
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les 70; Conservative
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ID _LAC2_RAT
AC P20767;
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"Structural rule of antibodies. Primary structure of a monoclonal "Structural rule of antibodies. Primary structure of a monoclonal rimmunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein Kern). V. The complete amino acid sequence and its genetic interpretation."; The complete amino acid sequence and its genetic interpretation."; The complete amino acid sequence and its genetic interpretation."; The CRIMINEDUS: THE CREGION OF THIS CHAIN HAS THE KERN+ MARKER.

-!- MISCELLANEOUS: THE IS A BENCE-JONES PROTEIN.

RISCP: PRO194; LAHUKN.

RISCP: 1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

RISCP: PRO196; IG-V.

RISCP: 1- MISCELLANEOUS: BENCE-JONES PROTEIN.

RISCP: PRO196; IG-V.

RISCP: 1- MISCELLANEOUS: BENCE-JONES PROTEIN.

RISCP: PRO196; IG-V.

RIMINARTY: SMO0406; IG-V: 1.

Immunoglobulin V region; Bence-Jones protein.

THOSULER 106 AA; 11277 MW; C884A05895B43CBE CRC64;
                                                                                                                                                                                                                              130 OPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                    2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                    30.6%; Score 380.5; DB 1; Length 104; 65.4%; Pred. No. 2.9e-24; Live 18; Mismatches 17; Indels 1.
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                                                                                            103 103 INTERCHAIN (WITH HEAVY CHAIN) 104 AA; 11318 MW; F087906DE43F7276 CRC64;
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106 106
106 AA; 11277 MW; C8B4AO5B9CB43CBE CRC64;
                                                                                                                                                                                                                                                                                                        190 SNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTEC 233
                                                                                                                                                                                                                                                                                                                                61 -GNKYIASSFLRLTAEQWRSRNSFTCQVTHEGNTVEKSLSPAEC 103
SMART; SM00407; IGC1; 1.

PROSITE; PS00290; IG MHC; 1.

Immunoglobulin domain; Immunoglobulin C region.

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DISULPID 103 103 INTERCHAIN (WITH H
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-IV region Kern.
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MEDLINE=71150336; PubMed=5549568;
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Best Local Similarity 65.4%
Matches 70; Conservative
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61 APVLVIYKDNERPSGIPERFSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYWVFGG 120
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1 MAWIPLLIPLITLCTGSEASYELTQPPSVSPGQTARITCSGDALPKQYAYWYQQKPGQ 60
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                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 24-9 kDa protein.
Hymo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-PRIMARY B-CELLS;
Straubborg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022823; AAH22823.1; -.
Hypothetical protein.
SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
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PRELIMINARY;
NCBI_TaxID=9606;
Query Match
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                                                          March 29, 2003, 09:06:23 ; Search time 21.223 Seconds (without alignments) 2271.829 Million cell updates/sec
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Q96:414 homo s
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Copyright (c) 1993 - 2003 Compugen_Ltd.
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                                                                                                                                                                  671580 seqs, 206047115 residues
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                                          - protein search, using sw model
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sp_bacteria:*
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sp_invertebrate:*
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sp_unclassified:*
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sp_bacteriap:*
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123 TRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LLITLIAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP 65
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 237;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR001596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
HYDChetical protein.
SEQUENCE 237 AA; 24897 MW; 73C7D70B8039D186 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 24.9 kDa protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 VLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LLG-LLSHCTGSGTSYVLTQPASVSVAPGQTARITCGGSNLGSKSVNWYQLRPGQAPILV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                      181 ETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUB-B-CELL;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007782; AAH07782.1;
InterPro; IPR003306; Ig.AHC.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00047; ig.2.
SNART; SM00408; IGC2; 1.
PROSITE; PS00178; AA_TRNA_LIGASE I; UNKNOWN_I.
PROSITE; PS00290; IGC4; UNKNOWN_I.
PROSITE; PS00200; IG_MHC; UNKNOWN_I.
SROWITE; AS00200; IG_MHC; UNKNOWN_I.
SROWITE; AS00200; IG_MHC; UNKNOWN_I.
SROWINGLOBULLIN domain.
SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.8%; Score 917.5; DB 4; Length Best Local Similarity 78.1%; Pred. No. 9.1e-75; Matches 178; Conservative 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020233, AAH20233.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UJN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 24,9 kDa protein.
                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown (protein for MGC:12849).
Homo sapiens (Human).
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                                                                                                                                                                                                                                          PRELIMINARY;
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TISSUE=TONSIL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBWUK4
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7

Gaps

9

Gaps

22;

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78 GDGIPDRFMGSSSGADRYLTLSNLQSDEAEYHCGESHTIDGQVGW------VFGGGTK 130
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                                                                                                                                                                                                                                                                                                                                                          74 PSGIPERFSGSKSGNTATLTINGVEAGDEADYYC-----QV-WDRASDHPVFGGGTR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 PILVIYDDSDRPSGIPERFSGS--KSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 PINMIYGDDLRPSGVSDRFSGSIDSSSNSAFLTIQNVQADDEADYYCQSY--SSGIRVFG 121
                                                                                                                                                                                                                                18 CALPVLTQPPSASAFLGASIKLTCTLSREHSSYTIEWYQQRPGRSPQYIMKVKSDGSHNK 77
                                                                                                                                                                                                             20 CAYE-LIQPPSVSVSPGQTARITCGGDNSRNEY-VHWYQQKPARAPILVIYDDSD----R 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 APLLLVFLHHLTGSCAQLVLTQPSSVSTSLGSTAKLPCKASTGNIGDSYVNWYQQYMGRS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGD--NSRNEYVHWYQQKPARA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                  Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                     185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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56.3%; Score 700; DB 11; Length 235
Best Local Similarity 60.7%; Pred. No. 3.6e-55;
Matches 142; Conservative 28; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.4%; Score 763; DB 4; Length 24 Best Local Similarity 67.4%; Pred. No. 7.8e-61; Matches 155; Conservative 20; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     191 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC002129; AAH02129.1; -.
HSSP; P01703; 7FAB.
                      Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 240 AA; 25977 MW; 921E47DDCA7259F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           099M11;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 25.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AA
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        InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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Q99M11
ID Q99M
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66 KVLIYGNYNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGAGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 RVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSR---NEYVHWYQQKPARAP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LLITLLAHCTGSWAQSVLAQPPSVSGAPGQTVTISCTGSSTNIGAGYAVHWYQQFPGAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical 26.0 kDa protein.

Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                       186 TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.9%; Score 856.5; DB 4; Length 236; Best Local Similarity 72.7%; Pred. No. 2.9e-69; Matches 168; Conservative 19; Mismatches 41; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 TTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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                                                  TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1;
Interpro; IRR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-TONSIL;
Straubberg R.;
Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020236; AAH20236.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 10, Last annotation update)
Unknown (protein for MGC:17259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                   126
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                                                                                                                              RESULT 5
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6; Gaps

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9; Сарв

121

유 ò RESULT 8 Q8TCJ5 ID Q8TC

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KRAIN-CS7BL/60; TISSUE-PANCREAS;

KRAIN-CS7BL/60; TISSUE-PANCREAS;

KRAMEN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Tawa M., Nishi K., Shoon H., Kasukawa T., Saito R.,

RA Aizawa K., Tawa M., Nishi K., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kadota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kichl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomitala M., Manger L., Washio T.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoembach C., Seya T., Shibata Y., Storch K.-F.,

M. Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S.,

Havashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                               119 FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
                                                                                                                                                                                                                                                                                                                                                                                             60 ARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHP-V 118
                                                                                                                                                                                                                                                                                                61 GKSPQLLVYNAKTLADGVPSRFSGSRSGTQFSLKINSLQPEDFGSYXCQ---HHSGIPFT 117
                                                                                                                                                                                                      1 MSVPTQVLGLLLCLTGARCDIQLTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQ 60
                                                                                                                                                                     1 MRVPAQLIGLLLLWLPGARCAYELTQ-PPSVSVSPGQTARITCGGDNSRNEYVHWYQQKP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 AGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.7%; Score 468.5; DB 11; Length 130; 68.5%; Pred. No. 1.1e-34;
                                                                        DB 11; Length 234;
                                                                      Query Match 38.6%; Score 479.5; DB 11; Length Best Local Similarity 42.4%; Pred. No. 2.6e-35; Matches 101; Conservative 46; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK007622; BAB25142.1; -. HSSP; P01842; 7FAB.
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Interpro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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1810027001RIK.
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Best Local Similarity
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                              GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
                                                       129 GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                          181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                      182 VETTQPSKQNNNKYMASSYLTLTAKAWETHSSYSCQVTHEGHTVEKSLSRADCS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LYMPH NODE;
Duceterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL713800; CAD28551.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019474; AAH19474.1;
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.v.
Pfam; PR0047; ig; 2.
SMART; SM00409; IGc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 44.3%; Score 551; DB 4; Length 10 Best Local Similarity 99.1%; Pred. No. 3.1e-42; Matches 105; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) U-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 11.3 kDa protein (Fragment).

DKF2EP67J0810.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
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TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                Q8TCJ5,
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Gaps

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115 DH--PVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YOOKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCOVWDRAS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSSPVKAGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRVPAQLLGLLLLMLPGARCAYELTOPP-SVSVSPGQTARITCGGDNS-----RNEYVHW 54
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.9 kba protein.
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 449.5; DB 11; Length 234; 41.6%; Pred. No. 1.3e-32; tive 43; Mismatches 87; Indels 9;
                                                                   TISSUE=COLON;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Rubmitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; PRO19760; AAH19760.1; -.
RINGEPRO; IPRO03599; Ig. C.1.
RINGEPRO; IPRO03599; Ig. C.1.
RINGEPRO; IPRO03566; Ig. YHC.
REMBL; SMO0407; IG; 2.
DR. SMART; SMO0407; IGG; 2.
DR. SMART; SMO0407; IGG: 1.
DR. SMART; SMO0407; IGG: 1.
DR. SMART; SMO0407; IGG: 1.
DR. SWART; SMO0407; IGG: 1.
DR. SWART; SMO0407; IGG: 1.
DR. SWART; SMO0407; IGG: 1.
SWART; SMO0407; IGG: 1.
DR. SWART; SMO0407; IGG: 1.
SWART; SMO0407; IGG: 1.
SWART; SMO0407; IGG: 1.
SWART; SMO0407; IGG: 1.
SWART; SMO0407; IGG: 1.
SWART; SMO0407; IGG: 1.
SWART; SMO0407; IGG: 2.
SWART; SMO0407; IGG: 2.
SWART; SMO0407; IGG: 2.
SWART; SWO0407; IGG: 2.
SWART; SWO0407; IGG: 2.
SWART; SWO0407; IGG: 3.
SWART; SWO0409; IGG: 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.2%; Score 462.5; DB 11; Length 41.4%; Pred. No. 9e-34; Antive 49; Mismatches 77; Indels
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Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (APR.-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH27418.1;
Hypothetical protein.
eroneNCE 234 AA; 25857 WW; 4EB08C81426AEAB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 41.68
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                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 RNEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Q8R062
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                                                                                                                                                                                               168 VAWKADSSPVKAGVETTTPSKOSNNKYAASSYLSLIPEQWKSHRSYSCOVTHEGSTVEKT 227
                                                                                                                                                                                                                                       QVWDRASDHPVFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 YOOKPARAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRAS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 SSPVKAG--VETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 NA-LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHVVYACEVTHQGLSSPVTKSFN 235
                7; Gaps
                                                                                                                                                63
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                                                                                                           QCW------VFGGGTKLTVLGQPKSSPSVTLFPPSSBELETNKATLVCTITDFYPGVVT
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OI-MAR-2002 (TEMBLrel. 20, Created)
OI-MAR-2002 (TEMBLrel. 20, Last sequence update)
OI-MAR-2002 (TEMBLrel. 20, Last sequence update)
OI-JUN-2002 (TEMBLrel. 21, Last annotation update)
Hypothetical 26.2 kDa protein.
Hypothetical (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; EC022362; AAH22362.1; -. Hypothatical protein. SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26, 2 kpa protein.
Homo sapiens (Human).
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37.3%; Score 464; DB 4;
Best Local Similarity 41.8%; Pred. No. 6.6e-34;
Matches 102; Conservative 52; Mismatches 74;
             14; Mismatches
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          Conservative
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TISSUE=LUNG;
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                                                                                                                                                                                                                                                                                                                                                                                              124 LSRADCS 130
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12.
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08VCI6
DD 08VCI6;
DT 01-MAR-;
DT 01-UJUN-;
DE HYPOTHER
OS MUS MUS COC MAMMALS
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OC MAMMALS
OC MAMMALS
OX NCBI TANA
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Q8TCD0;
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          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV-ETTTPSKQSNNKYAASSYLS 201
61 DGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATXYCQQY---SQFPFT 117
                                                                                      FGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 LTQPPSV-SVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILVIYDDSDRPSGIPERFS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LTQSPAIMSASPGERVTWTCSASSSVS-HMHWYQQKSGTSPKRWIYDTFKLTSGVPDRFS 84
                                                                                                                                                                                                    179 AGV-ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST--VEKTVAPTEC 233
                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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35.7%; Score 444; DB 11; Length 235;
Best Local Similarity 43.0%; Pred. No. 4.1e-32;
Matches 92; Conservative 45; Mismatches 69; Indels
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC, DMCNOWN 1.
PROSITE; PS002290; IG MHC; UNKNOWN 1.
SEQUENCE 235 AA; Z6021 MW; 5FC73BDBBD5E8FEF CRC64;
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01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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091W12
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AC 091W1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 DHP-VFGGGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKAD 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                Length 238;
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003509; Ig_cl.
R InterPro; IPR003006; Ig_like.
R InterPro; IPR003069; Ig_WHC.
R InterPro; IPR003596; Ig_W.
R Pfam; PF00047; ig; 2.
R SWART; SW00407; IG; 2.
R SWART; SW00410; IG; 2.
R SWART; SW00410; IG; 1.
R SWART; SW00410; IG like; 1.
R SWART; PF00590; Ig_WHC; UNKNOWN_1.
R PROSITE; PS00590; Ig_WHC; UNKNOWN_1.
R PROSITE; PS00590; Ig_WHC; UNKNOWN_1.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.5%; Score 441.5; DB 11; Length Best Local Similarity 40.7%; Pred. No. 7e-32; Matches 99; Conservative 49; Mismatches 80; Indels
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578 578 559 548 542.5
RESULT 1 S25756 Iq lambda chain - h
C;Species: Homo say C;Date: 22-Nov-1993 C;Accession: S25756 R;Combriato, G;; K]
Bur. J. Immunol. 21 A,Title: V(lambda) A,Reference number: A,Accession: S25756 A,Status: prelimina A,Molecule tyne: mR
A, Residues: 1-232 « A, Cross-references: C; Superfamily: immu C; Keywords: hetrot
F;14/-215/Domain: 11 Query Match Best Local Simila: Matches 196: Co
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DP
67
DD 66 VYDDSDRPS OV 127 VLGOPKAAP
125
Qy 187 SKQSNNKYA
  Db 185 SKQSNNKYA
RESULT 2
Ig lambda chain - hu C:Species: Homo san
C;Date: 22-Nov-1993 C:Accesion: 825747
R;Combriato, G.; Kl Eur. J. Immunol. 21
A; Ritle: V(lambda) A; Reference number:
A; Accession: S25747 A; Status: prelimina

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S69130 B49444 S725755 S17399 S17399 S17399 S12441 S12442 S12442 S12443 S12443 S12443 S12443 S12443 S12443 S12443 S12443	ALIGNMENT	ision 26- 991 C(lambda) 91257162; n not shc n not shc NID:93374 egion; im	Score 1016; D. Pred. No. 9.4e	VSVSPGQTA    :  :   VSVAPGKTA	ATLTINGVE      :    ATLTISRVE	NKATLVCLI          NKATLVCLI	HRSYSCOVT           HRSYSCOVT	RESULT 2 S25747 Ig lambda chain - human C; Species: Homo sapiens (man) C; Accession: 825747 R; Combriato, G: Klobeck, H.G. Eur. J. Immunol. 21, 1513-1522, 1991 A; Reference number: 816439; MUID:91257162; PA:Accession: 825747 A; Accession: 825747 A; Reference number: 816439; MUID:91257162; PA:Accession: 825747 A; Status: preliminary; translation not shown
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2016 2016 2017 2018 2017 2018 2019 1018 1018 1055		(man) 3 (man) 34, H.G. 5,8, H.G. 7(lambc) 739; M. transla 71,x5782 71,x5782	81.7% 86.0% vative	CAYELTO :      TSYVLTO	RFSGSKS         RFSGSNS	FPPSSEE	LSLTPEQ         LSLTPEQ	(man) quence k, H.G. 13-1525 J(lambd 439; MU
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818 799 639.5 635.5 635.5 602 603 600 578 578 578 578 578		a chain 22-Nov- 22-Nov- 22-Nov- 22-Nov- 22-Nov- 22- 22- 22- 22- 22- 23- 23- 23- 23- 23	datch ocal Sin 3 196;	7 LLGLLI        7 LLG-LI		VLGQPKAAPS		ULT 2 747. 747. 748. 749. 740. 740. 740. 740. 740. 740. 740. 740
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Gaps 61

12;

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Ricombriato, G.; Klobeck, H.G.

Bur. J. Immunol. 21, 1513-1522, 1991

A; Title: V(lambda) and J(lambda) -((lambda) gene segments of the human immunoglobulin lamk A; McGerence number: 816439; MUID:91257162; PMID:1904362

A; Accession: 825751

A; Accession: 825751

A; Accession: 525751

A; Conspecial type: mRNA

A; Molecule type: mRNA

A; Residues: 1-231 <COM>
A; Conspecial type: mRNA

A; Molecule type: mRNA

A; Conspecial type: mRNA

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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 GTKLTVLSQPKAAPSVTLFPPSSEBLQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
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A;Residues: 1-231 <COM>
A;Cross-references: EMBL:X57818; NID:g33735; PIDN:CAA40955.1; PID:g33736
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;146-214/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG
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PMID:1904362
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R;Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A,Title: V(lambda) and J(lambda)-C(lambda)
A,Reference number: S16439; MUID:91257162;
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Best Local Similarity 78.5%
Matches 183; Conservative
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S25753
Ig lambda chain - human
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C;Accession: S25751
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Matches 184;
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C'Abace: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C'Accession: 625738
R'Combriato, G.; Klobeck, H.G.
R'Combriato, G.; Klobeck, H.G.
A'Title: V(Lambda) and J(Lambda) -C(Lambda) gene segments of the human immunoglobulin lam A; Reference number: $16439; MUID:91257162; PMID:1904362
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                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:X57802; NID:g33701; PIDN:CAA40940.1; PID:g33702; Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
                                    A; Residues: 1-233 «COM»
A; Cross-references: EMBL:X57812; NID:g33723; PIDN:CAA40949.1; PID:g33724
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology «IMM»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LLWLP-----GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR
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                                                                                                                                                                                                                Length 233;
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78.8%; Score 979; DB 2; Length 23.
Best Local Similarity 80.3%; Pred. No. 2.7e-58;
Matches 187; Conservative 13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 233
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                                                                                                                                                                                                                                                                      20; Indels
                                                                                                                                                                                                          Query Match
Best Local Similarity 85.1%; Pred. No. 1.6e-60;
Matches 194; Conservative 13; Mismatches 20; ]
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Best Local Similarity
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                  Molecule type: mRNA
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A,Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of & A,Reference number: S04601; MUID:89296497; PMID:2500644
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C;Species: Home sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 82748
Eur. J. Immunol. 21, 1513-1522, 1991
Eur. J. Immunol. 21, 1513-1522, 1991
A;Fitle: V(Lambda) and J(Lambda)-C(Lambda) gene segments of the human immunoglobulin lamk
A;Reference number: 816439; MUID:91257162; PMID:1904362
A;Accession: 825748
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: 805270; 804601
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: 805270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726 C;Superfaaily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology cIMM>
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                                    183 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 213
204 PEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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A; Residues: 1-235 < KIS1>
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                                                                                                                                                                                                                                                                                      Ig lambda chain - human
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R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Takashi, I.; Shinoda, submitted to JIPID, November 1998

A;Description: Structural relationship of lambda type light chains with AL amyloidosis. A;Accession: JE0247
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                                                                                                                                                  Species: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LLTRCTVSEASYELTÓPPSGSVSPGKTÁRITCSGDALPKKYAYWYÓQKSGQSPVLVIYED 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X57810; NID:g33717; PIDN:CAA40947.1; PID:g33718 C;Superfantly: immunoglobulin V region; immunoglobulin homology C;Keywords: hererotetramer; immunoglobulin by F;141-209/Domain: immunoglobulin homology <IMM>
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82.9%; Pred. No. 1.3e-54;
Live 12; Mismatches 24; Indels
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A;Residues: 1.213 cALL:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;128-196/Domain: immunoglobulin homology <!MM>
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                                                                                                                  lambda chain - human (fragment)
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C;Species: Homo septens (man)
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C;Species: Homo septens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Combrato, G; Klobeck, H.G.
Bur. J. Immunod. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lamk
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Stecession: S25752
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Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 VLSOPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 185
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                                                                                                                                                                                                                                                                                                                                                                                                         6 LWLTLLTLCIGSVVSSELTQDPTVSVALGQTLRIKCQGDTIRSYYASWYQQKPGQAPTLL 65
                                                                                                                                                                                                                                                                                                   6; Gaps
                                                                                                                                                                                                                                                                                                                                                                  13 LWLP-----GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV 66
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                               A,Residues: 1.233 <CCM>
A,Residues: 1.233 <CCM>
A,Cross-references: BMBL:X57805; NID:g33707; PIDN:CAA40943.1; PID:g33708
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                    Length 233;
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                                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                                                                                                72.8%; Score 905; DB 2; 77.2%; Pred. No. 2.2e-53; live 15; Mismatches 31;
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ilarity 74.3%; Pred. No. 6.4e-52;
Conservative 21; Mismatches 36
                                                                                                                                                                                                                                    Query Match 72.89
Best Local Similarity 77.29
Matches 176; Conservative
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Matches 171; Conserv
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       A; Molecule type: mRNA
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cispecies: XEXOPECK, H.G.
K.Combriato, G.; Klobeck, H.G.
Bur. J. Immund, 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25742
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
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                                                                                                                                                                                                                                                                                                                                                                                              125 VTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT 184
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                                                                                                                                                                                                 6 LLITLIHCTGSWAQSVLTQPPSVSAAPGQXVTISCSGSSSNIGWNYVSWYQQLPGTAPK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 TPSKOSNNKYAASSYLSLTPEOWKSHRSYSCOVTHEGSTVEKTVAPTECS 235
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74.0%; Score 920; DB 2; Length 235; 77.4%; Pred. No. 2.3e-54; Live 15; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 910; DB 2; Length 232;
Pred. No. 1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Indels
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A, Status: preliminary; translation not shown
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Best Local Similarity 76.5%;
Matches 176; Conservative 1:
                                   Best Local Similarity 77.4%
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-232 < COM>
       Query Match
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Job time : 11.5021 secs
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S25757
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R;Combriato, G; Klobeck, Hg
R;Combriato, G; Klobeck, Hg
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lampa;Residues: S25757
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Accession: S25757
A;Coss-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology < IMM>
F;149-217/Domain: immunoglobulin homology < IMM>
C;Accession: $\frac{5}{5}750

R;Combriato, G.; Klobeck, H.G.

Bur. J. Inmunol. 21, 1513-1522, 1991

A;Title: V[lambda] and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: $16439; MUID:91257162; PMID:1904362

A;Accession: $25550

A;Accession: $25550

A;Residues: preliminary; translation not shown

A;Residues: preliminary; translation not shown

A;Residues: 1-25 < COM>
A;Residues: 1-25 < COM>
A;Residues: 1-25 < COM>
A;Cross-references: EMBL:X57815; NID:933729; PIDN:CAA40952.1; PID:933730

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;150-218/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                              70.9%; Score 881; DB 2; Length 235; 74.3%; Pred. No. 8.8e-52; Indels :ive 20; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.2%; Score 873; DB 2; Length 234; Best Local Similarity 72.6%; Pred. No. 3e-51; Matches 167; Conservative 25; Mismatches 36; Indels
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Best Local Similarity 74.3
Matches 171; Conservative
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Best Local Similarity
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S21066
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S21066
R;Dlouha, A.; Lecrotoisey, A; Henschen, A.; Ruttyn, Y.; Rouger, P.; Keil, B.
Protein Seq. Data Anal. 4, 319-134, 1991
A;Title: Partial amino acid sequence of the light chain of human anti-Rh(D) monoclonal ar A;Reference number: S21066; MUD:92253545; PMID:1812484
A;Accession: S21066
A;Status: preliminary
A;Accession: S21066
A;Residues: 1-213 - DLO>
A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 74-Thr & C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology < IMM>
F;128-196/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 FSGSKSGTSASLAITGLQAEDEGDYXCQIW----DYVVFGGGTKLIVLGQPKAAPSVTLF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 PPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYL 200
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
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1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478
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Sequence 71
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Compugen Ltd.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-296-005-14
US-09-296-005-16
US-08-466-151-8
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US-08-378-939-10
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US-08-458-516-13
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           GenCore version
Copyright (c) 1993 - 2003
                                                                         - protein search, using sw model
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seq length: 200000000
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Match
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Maximum DB E
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                                                                                                      Run on:
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US-08-487-550-8

Sequence 8, Application US/08487550

Patent No. 6113698

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION: IMMUNOSUPPRESANTS.

TITLE OF INVENTION: IMMUNOSUPPRESANTS.

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: OJUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 2561; DB 3;
Best Local Similarity 100.0%; Pred. No. 9.7e-199;
Matches 478; Conservative 0; Mismatches 0;
US-09-301-593-43

US-08-704-744-81

US-09-485-7378-67

US-09-485-7378-90

US-09-485-7378-90

US-09-487-7378-90

US-09-049-672A-4

PCT-US93-0783-23

US-07-934-373-623

US-07-934-375-23

US-08-437-6428-23

US-09-466-635-3

US-09-301-593-18

US-09-301-593-18

US-09-301-593-18

US-09-301-593-18

US-09-31-635-3

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US-09-31-635-3

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION UNDRER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acids
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Linear
TOPOLOGY:
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US-09-026-985-71
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US-09-027-449-71
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                                                                                                                                                                                                                                                                                                                                                                          | Sequence 71, Application US/09027449
| Sequence 71, Application US/09027449
| Patent No. 6025158
| GENERAL INFORMATION:
| APPLICANT: Gonzalez, Tania R. APPLICANT: Leong, Steven R. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Antibodies NUMBER OF SEQUENCES: 72
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Genented, Inc. STREET: 1 DNA Way
| CITY: South San Francisco STATE: California COUNTRY: USA
                      61 GKGPEWVGFIRNKPNGGTTEYAASVKDRPTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
   GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
                                                                       121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winbatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/027,449

FILING DATE: 20-Feb-1998

CLASSIFICATION ATA:

APPLICATION NUMBER: 60/074,330

FILING DATE: 22-Jan-1998

FILING DATE: 22-Jan-1998

PRIOR APPLICATION NUMBER: 60/038,664

FILING DATE: 21-Feb-1997

ATTOMEY/AGANT INFORMATION:

NAME: LOVE, RICHARD B.

REGISTRATION NUMBER: 9108FR3-2

REGISTRATION NUMBER: 9108FR3-2

TELERDACE/DOCKET NUMBER: P108FR3-2

TELERDACE/DOCKET NUMBER: P108FR3-2

TELERDALICATION INFORMATION:

TELEBHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
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US-09-027-449-71
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                                                                                                                                                                                                      Gaps
                                                                                     20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                          318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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                                                                                                                   1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYI--DPSNGET
                                                                                                                                                                                                                                                                                                                                                          198 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC
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Patent No. 6133426

GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                              11;
    Length 452;
                                              23; Indels
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Query Match

85.3%; Score 2184.5; DB 3;
Best Local Similarity 89.2%; Pred. No. 2.1e-168;
Matches 411; Conservative 16; Mismatches 23; ]
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Sequence 71, Application US/09234340A
Patent No. 646852
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Leonay, Steven R.
APPLICANT: Leonard G.
APPLICANT: Applicant Shahrokh, Zahra
APPLICANT: Applic General General APPLICANT: Tapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.2%; Pred. No. 2.1e-168;
Matches 411; Conservative 16; Mismatches 23;
              FILING DATE: 21-21
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION INFORMATION:
TELEPHONE: 650/225-5830
INFORMATION FOR SEQ 1D NO: 71:
SEQUENCE CHARACTERISTICS:
FEMANTH. 452 amino acids
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 452 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-121-952A-71
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US-09-234-340A-71
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Sequence 71, Application US/09121952A

Patent No. 6458355

GENERAL INFORMATION:
APPLICANT: Roumenis, Iphigenia
APPLICANT: Roumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra
APPLICANT: Sapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: MITH ANTI-IL-8 ANTIBODY FRACMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genenech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STREET: California
                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                        80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFBF 137
                                                                                                                                                                                                                                                                                                                                                 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 PPCPAPELLGGPSVPLFPPRFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291
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                                                                                                                                                                                                                                                                                                                                                                                                       138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
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                                                                                                                                                                      DB 4; Length 452;
                                                                                                                                                                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSKITVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 452
                                                                                                                                                            Query Match

85.3%; Score 2184.5; DB 4;
Best Local Similarity 89.2%; Pred. No. 2.1e-168;
Matches 411; Conservative 16; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/121,952A
                                                                  LENGTH: 452 amino acids
TYPE: Amino Acid
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                      TOPOLOGY: Linear
                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.8%; Score 2146.5; DB 4; Length 449; Best Local Similarity 88.3%; Pred. No. 2.5e-165; Matches 408; Conservative 12; Mismatches 25; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 FLYSKLIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 477
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; Sequence 2, Application US/09680148
; Patent No. 6417335
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241RLD1
; CURRENT APPLICATION NUMBER: US/09/680,148
                                                                                             GENERAL INCORNATION:
APPLICANT: BASEY, CAROL D.
APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILLS OF INVENTION: PROTEIN PURIFICATION
CURRENT FILING DATE: 2000-10-03
CURRENT FILING DATE: 2000-10-03
PRIOR PILING DATE: 1998-05-06
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
SEQ ID NO S.
                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Sequence is synthesized. US-09-679-397-2
                                                                Sequence 2, Application US/09679397
Patent No. 6339142
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 449
                                                 US-09-679-397-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.3%; Score 2184.5; DB 4; Length 452; 89.2%; Pred. No. 2.1e-168; Live 16; Mismatches 23; Indels 11;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/234,340A
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION: NAME: LOVE, Richard B. REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 34,659
TELEPHONE: 650/255-5530
TELEPHONE: 650/255-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
              ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                 CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.2'
Matches 411; Conservative
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-234-340A-71
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DB 1; Length 459;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: TITUG, MARLANA K
REGISTRATION NUMBER: 9437/204199
TELEPHONE: 202-861-371
TELEPHONE: 202-81-371
TELEPHONE: 202-81-371
TELEPHONE: 202-81-371
TELEPHONE: S02-81-371
TELEPAS: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
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US-08-887-352B-18
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| Sequence 7, Application US/08157101A
| Patent No. 5808032
| GENERAL INFORMATION:
| APPLICANT: KURIHARA, TATSUYA
| APPLICANT: MISHIHARA, TATSURO
| APPLICANT: NISHIHARA, TATSURO
| APPLICANT: NISHIHARA, TATSURO
| TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
| TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
| TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
| TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
| TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
| TITLE OF INVENTION: 9 PLASMIDS THEREFOR
| NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
| ADDRESSEE: PILLSBURY, MADISON & SUTRO
| STREET: 1100 NBW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.8%; Score 2146.5; DB 4; Length 449; 88.3%; Pred. No. 2.5e-165; Ative 12; Mismatches 25; Indels 17;
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                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Sequence is synthesized.
Patent No. 6417335
US-09-680-148-2
                      CURRENT, FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
LENGTH: 449
                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.3%
Matches 408; Conservative
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US-08-157-101A-7
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Sequence 18, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
<u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                          231 SCDKTHTCPPCPAPELLGGPSVFLFPPKPTLMISKTPEVTCVVVDVSHEDPEVKFNWY 290
                                                                                                                                                               71 RNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVC 130
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Gaps
                                                                                  11 VAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFI 70
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Gape

197 170 257 230 290

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79 TEYAASUKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.4%; Score 2135; DB 4; Length 4
Best Local Similarity 88.5%; Pred. No. 2.1e-164;
Matches 408; Conservative 14; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                          NAME/KEY: Artificial
LOCATION: 1-451
COTHER INFORMATION: Heavy chain sequence derived from MAB11
MS-09-108-207C-18
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US-09-282-505-2
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; GENERAL INFORMATION:
; APPLICANT: BSONE Ekinaduese Idusogie et al.; TILE OF INVENTION: Polypeptide Variants; TILE REFERENCE: P1266R1; CURRENT APPLICATION NUMBER: US/09/282,505A; CURRENT FILING DATE: 1999-03-31
CURRENT APPLICATION NUMBER: US/09/109,207C CURRENT FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR FILING DATE: 1997-07-03 NUMBER OF SEQ ID NOS: 44 LENGTH: 451
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LOCATION: 1-451
                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial
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1S-09-109-207C-18
1S-09-109-207C-18
1S-09-109-207C-18
2Squence 18, Application US/09109207C
3 Patent No. 617213
3 GENERAL INFORMATION:
3 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
3 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
3 FILE REFERENCE: P1123R1
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Best Local Similarity 88.5%; Pred. No. 2.1e-164;
Matches 408; Conservative 14; Mismatches 27; Indels 1
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VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC
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Patent No. 6290957
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 408; Conservative
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Best Local Similarity
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US-09-296-005-18
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          Length 451;
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      ; Score 2135; DB 4; Length 4; Pred. No. 2.1e-164; 14; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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83.4%; Score 2135; DB 4;
Best Local Similarity 88.5%; Pred. No. 2.1e-164;
Matches 408; Conservative 14; Mismatches 27;
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TITLE OF INVENTION: Polypeptide Variants; FILE REPERBENCE: PIZe6
CURRENT APPLICATION NUMBER: US/09/054,255; UWRENT FILING DATE: 1998-04-02; NUMBER OF SEQ ID NOS: 2
LENGTH: 451
         83.4%;
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                                Matches 408; Conservative
                     Similarity
     Query Match
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                    Local
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides FILE REFERENCE: Pli23Clr
CURENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER APPLICATION NUMBER: US 08/887,352
SEALIER PILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 18
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COTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-296-005-18
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88.5%; Pred. No. 2.1e-164;
rative 14; Mismatches 27;
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US-08-887-352B-16

Sequence 16, Application US/08887352B

Sequence 16, Application US/08887352B

Patent No. 59945101

Patent No. 59945101

Patent No. 59945101

TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
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                                                                                                                               438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                        411 YSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 451
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Uul-1997
FILING DATE: 03-Uul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 191123
TELEPHONE: 650/225-1489
TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 408; Conservative 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.2%; Score 2132; DB 2;
88.5%; Pred. No. 3.7e-164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-3528-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DNA Way
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Best Local Similarity
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                                                                                                                                                                                                               Sequence 14, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: I DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
  351 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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83.2%; Score 2132; DB 2; Length 451;
Best Local Similarity 88.5%; Pred. No. 3.7e-164;
Matches 408; Conservative 13; Mismatches 28; Indels 1:
                                                                      438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                             411 YSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENI INFORMATION:
NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFRENCE/DOCKET NUMBER: 91123
TELEPHONE: 650/225.1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: Linear
US-08-887-3528-14
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Sequence 52, Appl
Sequence 52, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 16, Appl
                                                                                          March 29, 2003, 09:14:52 ; Search time 18.3244 Seconds
  (without alignments)
1531.829 Million cell updates/sec
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Sequence 66, Appli
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Sequence 8, Appli
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Sequence 71, Ar
Sequence 26, A
                                                                                                                                                        US-09-758-173-8
2561
1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-736-371B-21

US-09-825-012-46

US-09-825-012-55

US-09-825-012-61

US-09-825-012-61

US-09-825-012-61

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US-09-920-171-14

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US-09-802-096-8
US-09-925-179-66
                                                                                                                                                                                                                                                                            237916 seqs, 58723674 residues
                                                           OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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        US-09-925-179-68
        Sequence 68, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37,
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## ALIGNMENTS

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RESULT 1

US-10-124-905-8

1 Sequence 8 Application US/10124905

1 Patent No. US20020166136A1

1 GENERAL INFORMATION

1 TITLE OF INVERTION: "MONEY WONCLONAL ANTIBODIES SPECIFIC

1 TITLE OF INVERTION: "MONEY WONCLONAL ANTIBODIES SPECIFIC

1 TITLE OF INVERTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

1 TITLE OF INVERTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

1 TITLE OF INVERTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

1 TITLE OF INVERTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

1 TITLE OF INVERTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

2 CORRESPONDENCE, ADDRESS;

3 CORRESPONDENCE, ADDRESS;

4 COMPUTER READABLE FORM:

5 STATE: VA

COMPUTER READABLE FORM:

5 SOTTWARE: PROPEY disk

COMPUTER READABLE FORM:

5 SOTTWARE: PROPEY DISK

5 CONTAINING SYSTEM: PC-OOS/MS-DOS

5 SOTTWARE: PS-OOS/MS-DOS

5 CURRENT APPLICATION DATA:

5 FILING DATE:

6 FILING DATE:

7 FILING DATE:

7 FILING DATE:

7 FILING DATE:

8 FORTAL TOWN UNMERR: 09/383,916

7 FILING DATE:

8 FORTAL TOWN UNMERR: 03-016

8 REFERENCE/POCKAR UNMERR: 03-036-6620

7 TELEFRAX: 703-636-6620

7 TEL
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                         TOPOLOGY:
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US-09-948-429B-8
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Patent No. US20020177689A1

CENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
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                                                                                                                                                                                                                                                           61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
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                                                                                                                                                                                                      1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                                                                                                                                                  Gaps
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0
                                                                                                             Length 478;
                                                                                                                                                Indels
                                                                                                         100.0%; Score 2561; DB 9;
100.0%; Pred. No. 1.4e-129;
ative 0; Mismatches 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
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APPLICATION'NUMBER: US 08/487,550
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. rYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-8
                                                                                                         Query Match
Best Local Similarity 100.
Matches 478; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-948-429B-8
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; Sequence 71, Application US2003002190A1
; Sequence 71, Application No. US2003002190A1
; Publication No. US2003002190A1
; APPLICANT: Genentech, Inc., Hsei, Vanessa APPLICANT: Leong, Steven R.
; APPLICANT: Shahrokh, Zahra APPLICANT: Shahrokh, Zahra APPLICANT: Shahrokh, Zahra APPLICANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: ApplicANT: Applic
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100.0%; Score 2561; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.4e-129;
Matches 478; Conservative 0; Mismatches 0;
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
FEFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAN: 703-836-6620
INFORMATION FOR SEQ 10 NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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TITLE OF INVENTION: WUCIN-1 Specific Binding Members and Methods of Use Thereof FILE REFERENCE: DYX-015.1 US
CURRENT APPLICATION NUMBER: US/09/822,698A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US/09/538,913
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Microsoft Word
SEQ ID NO 26
LENGTH: 451
        APPLICANT: Henderikx, Maria P.G.
                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.3%; Score 2184.5; DB 9; Length 452; 89.2%; Pred. No. 1.5e-109; ative 16; Mismatches 23; Indels 11;
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ZIP: 94080
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/094003
APPLICATION NUMBER: 60/094003
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, KIChard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R4-1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                              SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPE. Amino Acid
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Best Local Similarity 89.2%
Matches 411; Conservative
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Sequence 26, Application US/09822698A Patent No. US20020146750A1 GENERAL INFORMATION:
APPLICANT: Hoogenboom, Hendricus R.J.M.

US-09-822-698A-26

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                                                                                                                                                                      ; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1 US-09-822-698A-26
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69
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US-09-736-371B-21
Sequence 21, Application US/09736371B
Fatent No. US20020131968A1
GENERAL INFORMATION:
APPLICANT: Waldmann, Herman
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
FILE REFERENCE: Waldmann
CURRENT PAPLICATION NUMBER: US/09/736,371B
CURRENT PILING DATE: 2002-04-25
FRIOR FILING DATE: 1998-07-21
FRIOR APPLICATION NUMBER: 9815909.8
FRIOR FILING DATE: 1999-07-21
FRIOR FILING DATE: 1999-07-21
SROFTWARE OF SEQ ID NOS: 30
SOFTWARE: PALENTING DATE: PROSTERING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTING PARTI
TYPE: PRT
ORGANISM: artificial sequence
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170 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 229
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                       181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
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                                                                             121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
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TITLE OF INVENTION: Compounds for Targeting
FILLE REFERENCE: 43191-256808
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
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Patent No. US20020122798A1
GENERAL INFORMATION:
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SEQ ID NO 55
LENGTH: 741
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84.9%; Pred. No. 1.7e-107;
iive 21; Mismatches 40; Indels 11;
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                                                                               Length 449;
                                                                                 Query Match

84.1%; Score 2154; DB 10; Length 4

Best Local Similarity 89.5%; Pred. No. 6.1e-108;

Matches 411; Conservative 9; Mismatches 29; Indels
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Sequence 46, Application US/09825012
Patent No. US2002012798A1
GENERAL INFORMATION:
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
CURRENT FILING DATE: 2001-04-03
PRIOR PELICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VARIABE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VARIABE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VARIABE: 2000-04-03
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.9
Matches 406; Conservative
                         ORGANISM: Homo sapiens US-09-736-371B-21
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                                                                                RESULT 9
US-09-825-012-61
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KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
                230 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 289
                                                            DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
                                                                                                                                            170 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT 229
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84.9%; Pred. No. 3.1e-107;
tive 21; Mismatches 40; Indels 11;
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                                                                                                                                                                                                                                                                                            Sequence 52, Application US/09825012
Patent No. US20020122798A1
GENERAL INFORMATION:
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 41191-256808
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
SEQ ID NO 5.2
LENGTH: 729
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ORGANISM: Artificial Sequence
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US-09-825-012-52
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; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-61
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84.9%; Pred. No. 3.1e-107;
:ive 21; Mismatches 40;
                                                                                                                                                                    Sequence 61, Application US/09825012
Patent No. US2002012798A1
GENERAL INFORMATION:
APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808
CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-03
SPIOR PILING DATE: 2000-10-03
SPIOR PILING DATE: 2000-10-03
SOFWARE: Patentin version 3.1
SEQ ID NO 61
LENGTH: 739
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US-09-825-012-49
; Sequence 49, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
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; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion US-09-825-012-58
ORGANISM: Artificial Sequence
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US-09-920-171-18
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; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-49
                                                                                                                                                                                                                                                                                                         83.5%; Score 2138.5; DB 10; Length 84.9%; Pred. No. 6.4e-107; Live 21; Mismatches 40; Indels
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APPLICANT: Young, Robert; TITLE OF INVENTION: Compounds for Targeting; FILE REFERENCE: 43191-256808; CURRENT FILING DATE: 2001-04-03; PRIOR APPLICATION NUMBER: US 60/237,159; PRIOR APPLICATION NUMBER: GR 0008049:9; PRIOR PILING DATE: 2000-04-03; NUMBER OF $EQ ID NOS: 102; NUMBER OF $EQ ID NOS: 102; SEQ ID NO 58; LENGTH: 740; TYPE: PRI **
             CURRENT APPLICATION NUMBER: US/09/825,012
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/237,159
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: GB 0008049.9
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
 FILE REFERENCE: 43191-256808
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Matches 404; Conservative
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Best Local Similarity
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Query Match 83.5%; Score 2138.5; DB 10; Length 740; Best Local Similarity 84.9%; Pred. No. 6.5e-107; Matches 404; Conservative 21; Mismatches 40; Indels 11;
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APPLICANT: Desta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P113352US
CURRENT APPLICATION UNDRER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
FRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 18
LENGTH: 451
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US-09-920-171-18
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171 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC 230
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Fatent No. US20020054878A1
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P1123C2US
CURRENT PAPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
PRIOR PAPLICATION NUMBER: US/08/887,352
PRIOR APPLICATION NUMBER: US/09/920,171
PRIOR APPLICATION NUMBER: US/09/920,171
PRIOR APPLICATION NUMBER: US/09/920,171
PRIOR APPLICATION NUMBER: US/09/920,171
PRIOR APPLICATION NUMBER: US/09/920,005
PRIOR SEQ ID NOS: 44
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US-09-920-171-14
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ORGANISM: Artificial Sequence
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LENGTH: 451
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US-09-925-179-65
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VHTPPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
FILE REFERENCE: PO118P2CIDICIUS
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-06-14
PRIOR FILING DATE: 1992-06-14
PRIOR FILING DATE: 1992-06-14
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 65
LENGTH 451
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83.2%; Score 2132; DB 9;
Best Local Similarity 88.5%; Pred. No. 9.2e-107;
Matches 408; Conservative 13; Mismatches 28;
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Publication No. US20030044858A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
FEATURE:
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TEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYG-GYFEF 137
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                                                                                                                                               291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
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                                                                                                                   AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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Sequence 16, Application US/09920171
Sequence 16, Application US/09920171
Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Seque
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Best Local Similarity 88.5%; Pred. No. 9.2e-107;
Matches 408; Conservative 13; Mismatches 28; Indels 12
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, OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16
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ORGANISM: Artificial Sequence
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## ALIGNMENTS

Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; freatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; Macaque primatized 7B6 heavy chain protein. AAW63763 standard; Protein; 478 AA Hanna N; 96US-0746361 97WO-US19906 29-SEP-1998 (first entry) (IDEC-) IDEC PHARM CORP Anderson DR, Brams P, cell proliferation WPI; 1998-286601/25. N-PSDB; AAV35487. Macaca fascicularis 29-OCT-1997; 08-NOV-1996; WO9819706-A1 14-MAY-1998.  Human, macaque monkey; light chain, primatised antibody, 786 antibody, neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; mutein.

Chimeric - Homo sapiens. Chimeric - Macaca sp.

WO200189567-A1 29-NOV-2001

Synthetic.

Protein sequence of primatised form of the heavy chain of 7B6 antibody

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This sequence represents a primatized form of the antibody 7B6 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. Host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunosupens, can also be used as imaging agents and as vaccines or immunosupersessants. Aloky in the proteins or shulders long-term, antigen-specific immunosuppression, i.e. it inhibits production of interlukin-2. (T.), real proliferation and
New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of interleukin-2 (IL-2), T cell prolife
antigen-specific immunoglobulin G (IgG) responses
                                                                                            cells, e.g. graft rejection or tumours
                                                                                                                                                 Example 7; Fig 4b; 87pp; English.
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478 AA; Sequence CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as

Example 8; Fig 4b; 89pp; English.

monoclonal antibody which specifically binds to B7.1 antigen

N-PSDB; AAS17245

Use of

Р, Brams

22-MAY-2000; 2000US-0576424. 22-MAY-2001; 2001WO-US16364

(IDEC-) IDEC PHARM CORP Anderson DR, Hanna N, WPI; 2002-089895/12

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AAU11644 standard; Protein; 478 AA

12-MAR-2002 (first entry)

AAU11644;

RESULT 2
AAU11644
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is concer where B calls promote the growth and/or metastasis of tumours, a cancer where B calls promote the growth and/or metastasis of tumours, B call lymphoma, B call lymphoma, B call lymphoma, a cancer where B calls promote the growth and/or metastasis of tumours, C cancer where mellitus, rheumatoid arthritis, psoriasis of tumours, cype I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammancy bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive disease, intestinal inflammations and allergies e.g. migraine, disease and ulcerative collitis, food-related allergies e.g. migraine, sequence represents the havy chain of 786, a primatised antibody
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2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7B6. Cloned 7B6 light and heavy variable genes (see also AAT62511 and AAT13847) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. Of the primatised antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01817-19 and AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
PPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                              KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; cynomolgus monkey; macaque; 7B6; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                               Primatised anti-human B7.1 antigen antibody 7B6 heavy chain.
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                                                                                                                                                                                                                                                                                                                      AAW01820 standard; Protein; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 9B; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US10053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brams P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-108638/10.
N-PSDB; AAT13847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody; HV-neutralising monoclonal antibody; immunoglobulin; AIDS; acquired immune deficiency syndrome; chimeric antibody; surface glycoprotein gp120; V3 loop.
                                                                         1 MGWSLILLEFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                            61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
                                                                                                                                                                                   121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                                                                                       PPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                                                                                                                                                                                                                                                              KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                       1 MGWSLILLFLVAVATRVQCEVQLVESGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                  YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
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                            ö
    Length 478;
                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-HIV-1 recombinant antibody 447-52D heavy chain,
 99.8%; Score 2555; DB 18; 99.8%; Pred. No. 1.1e-151; ive 0; Mismatches 1;
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Query Match
Best Local Similarity 99.8'
Matches 477; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MERI ) MERCK & CO INC. (JOHN/) JOHNSON L S. (PFAR/) PFARR D S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conley AJ, Emini EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-336600/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 377
                                                                                                                                                                                                                                                                                          EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRG--GVCYGGYFEF 137
                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                           Gaps
                                                      EBV-transformed cell lines and mouse-human heterohybridomas producing human MAbs specific for the gp120 V3 loop of HIV-1 MN isolate were obtained. MAb 447-52D was found to recognise the tetrapeptide motif GPGK, i.e. the Principal Neutralising Determinant common to the V3 loop of different HIV isolates. A recombinant Ab was produced in which the H chain V region was derived from 447-52D and to which a signal sequence and a H chain intronic sequence are appended, fused to a fragment coney. a short intronic segment of the human gamma 1 C region and the human gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8; diagnosis; inflammatory disorder; conjugate; immunoglobulin;
                                                                                                                                                                                                                                                                                                      PPCPAPELLGGBSVFLFPKDKDTLMISRTPBVTCVVVDVSHEDPBVKFNWYVDGVEVHN
                                                                                                                                                                                                                                               20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT
                                                                                                                                                                                                                                                            1 EVQLVESGGGLVKPGGSLRLTCVASGFTFSDVWLNWVRQAPGKGLEWVGRIKSRTDGGTT
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   or treating
                                                                                                                                                                                                                           5
                                                                                                                                                                                                   85.8%; Score 2197; DB 14; Length 461; 90.2%; Pred. No. 2.4e-129; ive 14; Mismatches 29; Indels 2
   least two isolates, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 YSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 461
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                                                                                                                                                          encoding domain in its genomic form
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                                   Example 9; Fig 2A; 154pp; English
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                infection in diagnosis, etc.
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                                                                                                                                                                                                                  Best Local Similarity 90.2
Matches 416; Conservative
                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                 461 AA;
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antibody fragments covalently attached to one or more nonproteinaceous polymer molecules, where the apparent size of the conjugate is at least about 500 kpa. Conjugates of antibody fragments which bind the human interleukin (IL) 8 with a nonproteinaceous polymer can be used for treating inflammatory disorders e.g. acute lung injury, ischaemic reperfusion disorder, and autoimmune diseases. They can also be used for treating e.g. inflammatory skin diseases including psoriasis and atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases. The conjugates can also be used as reagents in an animal model system for in vivo study of the biological functions of the antigen recognised by the conjugate. The present sequence represents a recombinant immunoglobulin protein from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a novel conjugate having one or more
                                                                                                                                                                                                                                                                                                                                                                New conjugates of nonproteinaceous polymers with antibody fragments, used for treating inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVXYC-----ARGDYRYNGDWFFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYI--DPSNGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.3%; Score 2184.5; DB 20; Length 452;
89.2%; Pred. No. 1.4e-128;
tive 16; Mismatches 23; Indels 11;
                                                                                                                                                                                                                                      Ñ
                                                                                                                                                                                                                                      Shahrokh
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                                                                                                                                                                                                                                         Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 354-355; 360pp; English
                                                                                                                                                                                                                                         SJ,
                                               98US-0122513.
98US-0012116.
98WO-US03337.
98US-0121952.
                                                                                                                                                                                                                                         Leong
99WO-US01081
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                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                         Koumenis I,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 WPI; 1999-469134/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 AA;
19-JAN-1999;
                                                                                                                             24-JUL-1998;
                                                  24-JUL-1998;
22-JAN-1998;
                                                                                                      20-FEB-1998
                                                                                                                                                                                                                                                                  Zapata GA;
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The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 6G4.2.5V1N35A light chain; and amino acids 24-253 of the humanized anti-IL-8 6G4.2.5V1N35A heavy chain. The anti-IL-8 MAbs and fragments and be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic acids encoding the anti-IL-8 MAb can be associated in a vector with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule encodes a polypeptide which is an anti-interleukin-8 monoclonal antibody or antibody fragment useful for the production of anti-interleukin-8 monoclonal antibodies or fragments
292 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4V11N35A;
inflammatory disorder; adult respiratory distress syndrome;
affinity purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     another gene encoding another protein or protein fragment to produce fusion protein which can make isolation and/or purification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT 79
                                                                          352 QVYILPPSREEMTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFL
                                             378 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised anti-IL-8 antibody related protein seg ID No:71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Indels
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                                                                                                                                    438 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                 412 YSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.3%; Score 2184.5; DB 21
89.2%; Pred. No. 1.4e-128;
ive 16; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examples; Columns 199-202; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gonzalez TN;
                                                                                                                                                                                                                                                                                                 AAY77766 standard; Protein; 452 AA
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98US-0074330,
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                                                                                                                                                                                                                                                                                                                                               AAY77766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of humanised monoclonal anti-IL-8 antibodies which can be used in the diagnosis and treatment of inflammatory disorders, including adult respiratory distress syndrome, septic shock, multiple organ failure, bacterial pneumonia and inflammatory bowel disease. The present sequence comprises one of the
                                                                                                                                                                                                                                       Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock; adult respiratory distress syndrome; multiple organ failure; bacterial pneumonia; inflammatory bowel disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized anti-interleukin 8 monoclonal antibody variant useful for treating inflammatory disorders, such as adult respiratory distress syndrome, hypovolemic shock and ulcerative colitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 WGOGTLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGGLVKDYFPEPVTVSWNSGALTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPBVKFNWYVDGVEVHN
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89.2%; Pred. No. 1.4e-128;
tive 16; Mismatches 23; Indels 11;
                                                                                                                                                                                            Humanised anti-IL-8 antibody related protein SEQ ID NO: 71.
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                                                       AAB30322 standard; Protein; 452 AA
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98US-0074330.
                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                    human rabies-immune globulin; monoclonal; virucide; heavy chain; monoclonal rabies virus neutralising antibody; immunoglobulin; chain; central nervous system; CNS; prophylactic therapy; clone JA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the heavy chain protein of the monoclonal antibody from clone JA. The invention relates to an isolated human monoclonal rables vitus neutralising antibody (virucide) derived from cDNA clones encoding the antibody heavy and light chains expressed in heterologous expression systems and purified away from deleverious contaminancs. The invention provides a fused gene encoding a chimeric immunoglobulin light chain and a fused gene encoding a chimeric immunoglobulin heavy chain. The antibody of the invention is useful for
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59 TYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYC-----ARGDYRYNGDWFFDV 111
                                   197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human monoclonal rabies virus neutralising antibody useful for treating individual exposed to rabies virus and for preventing spread of rabies virus to central nervous system -
                                                                                                                                                                              112 WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                                                                                                                       PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                     PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRBP
                                                                                                                                                                                                             QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                              VHTPPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC
                                                                                                  172 VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
                                   WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                                                                                                                                                                                                                                                                                                                                                                                                  Heavy chain protein of the monoclonal antibody from clone JA.
                                                                                                                                                                                                                                                        YSKLIVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                   YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 23-24; 25pp; English.
                                                                                                                                                                                                                                                                                                                                   AAO14065 standard; Protein; 474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2000; 2000US-204518P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dietzschold B;
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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treating an individual exposed to a rabies virus by administering to the individual a therapeutically effective amount of the antibody, and preventing a spread of the rabies virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious post-exposure prophylactic therapy for individuals exposed to a rabies virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antivitral; antibacterial; antialergic; dermatological; hamostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356
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                                                                                                                                                                                                                                                                                                                                                                                                             61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCT-- 118
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                          293 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMHBALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                        1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                                                                                                           1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 REVIMIVVLNGG------FDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
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                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                      Length 474;
                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                         85.2%; Score 2183; DB 23;
86.7%; Pred. No. 1.8e-128;
iive 18; Mismatches 34;
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                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.74
Matches 418; Conservative
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The invention relates to polynuclectides encoding novel human

The invention relates to polynuclectides encoding novel human

Expectation or their active domains. The polypeptides, polynuclectides and

antibodies raised against the polypeptides caused in a method of

treatment of a mammal and prevention of disorders caused by the aberrant

protein expression or activity. The polypeptides can be used as

CC molecular weight markers, food supplements, and in antibody production.

The polypeptides are used to identify compounds which bind to the

polypeptides. Polynucleotides of the invention are used as probes and

primers, for sequencing, for chromosome or gene mapping, in the

production of recombinant proteins, and in generating anti-sense DNA or

RNA and in gene therapy. Polypeptides of the invention can be used to

target drugs to a tumour, in assays to determine biological activity, to

crafget drugs to a tumour, in assays to determine biological activity, to

raise antibodies/elicit an immune response, to determine quantitative

protein levels, as tissue markers, and to isolate receptors or ligands.

CC raise for the proliferantial may also be useful in treating platelet

disorders, stem call disorders, reconstanting burns, promoting

CC ligament and/or nerve tissue, wound healing, treating burns, promoting

CC ontraceptive, treating osteoporosis and osteoarthritis, an anemia,

CL and polyment and autoimmunity, cancerthing from bacterial, viral or

Graft-versus-host diseases, nervoses, and infection.

CH and inflammatory diseases, eczema, allersy, asthma,

CC antiliammatory diseases, eczema, heamophilia, thrombosis,

The proliamman servose system disorders, and infection.
                                                                                                                                                                                                                                                                        Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEFGLSWVFLVALLRGYQCQVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
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                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 611-612; 894pp; English.
                                                                                                                                              Tang YT, Liu C, Drmanac RT,
25-JAN-2001; 2001WO-US02623
                                                 25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 85.6%
Matches 416; Conservative
                                                                                                                                                                                                  2001-451939/48.
                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                       N-PSDB; AAS22593
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17; Gaps 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60 85.0%; Score 2177.5; DB 22; Length 477; 85.6%; Pred. No. 4e-128;

GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSIKIEDTAVYYCTTS 120 121 YISHCRGG-----VCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAA 172 171 ઠે g ò a

352 VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKC 351 353 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 412 **WWDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC** . 262 293

471 412 BSNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 352 KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK 478 472 SLSPGK 477 413 473 RESULT 10 AAW69316 g ð ద ò

Anti-IL-8 humanised antibody 6G4V11N35A.choSD.9. AAW69316 standard; Protein; 452 AA. (first entry) 15-FEB-1999 AAW69316;

Humanised antibody; chimeric antibody; monoclonal antibody; mouse; human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis; inflammatory bowel disease; Crohn's disease; ulcerative colitis; ischaemic reperfusion; adult respiratory distress syndrome; dermatitis; meningitis; encephalitis; uveitis; autoimmune disease; rheumatoid arthritis; Sjorgen's syndrome; vasculitis; trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis; vasculitis; bronchitis; bronchitectasis; cystic fibrosis; diagnosis; therapy; 6G4VIIN35A.choSD.9.

Chimeric - Mus sp. Chimeric - Homo sapiens 20-FEB-1998; WO9837200-A2 27-AUG-1998. 

98US-0012116. 97US-0804444. 98WO-US03337 2-JAN-1998; 21-FEB-1997;

(GETH ) GENENTECH INC

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Koumenis I, Leong SR, Presta LR, Shahrokh Z; Zapata GA; нвеі V,

WPI; 1998-467563/40. N-PSDB; AAV44956.

New conjugates of antibody fragments - having covalently attached non-proteinaceous polymer molecules, particularly polyethylene glycol, for improving the residence time in the circulation.

Example P; Fig 48A-Z; 328pp; English

This polypeptide is encoded by vector plasmid p6G4V11N35A.choSD.9 (see AAV44956). It comprises a humanised 6G4V11N35A IgG containing complementarity determining regions of murine anti-interleukin-8 (IL-8) mnoclonal antibody [MAD) 6G5.2.5 (see AAW69301-04) in a human template. Humanised anti-IL-8 MADS (see AAW69301-04) are described for use in diagnostic applications and in the treatment of inflammancy disorders. The invention provides conjugates of an antibody fragment and a polymer, such as PEG, that have improved half-life, mean residence time, and/or clearance rate. The conjugates can be used for immune therapy of e.g. psoriasis, responses associated with inflammatory bowel disease (such as Conjugates and ulcerative collitis), ischemic reperfusion, adult respiratory distress syndrome, dermatitis, meningitis, and encephalitis, uveitis, autoimmune diseases such as rheumatoid

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셤 ે 엄 us-09-758-173-8.rag

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Steindl
                                       135..145
/label= Framework_4
146..475
/label= Constant_region
                                                                                                                                                                                        Kohl J,
 86..117
/label= Framework_3
118..134
                                                                                                                                                                                                                                                                               Claim 2; Page 24; 52pp; German.
                           /label= CDR_3
                                                                                                                             91WO-1000067
                                                                                                                                                  90AT-0001178
                                                                                                                                                                                       Felgenhauer M, Himmler G,
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.2
Matches 417; Conservative
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N-PSDB; AAQ20066.
                                                                                                                                                                     (JUNG/) JUNGBAUER A.
                                                                                                                                                                                                                                                                                                                                                           475 AA;
                                                                                                                               28-MAY-1991;
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                                                                                         WO9118983-A.
                                                                                                             12-DEC-1991
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                                                                                                                                                                                                                                   231
                                                                                                                                                                                                                                                                                                   PPCPAPELLGGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 317
                                                                                                                                                                                                                                                                                                                                                     EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGG--YFEF 137
                                                                                                                                                                                                                       138 WGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 197
                                                                                                                       Gaps
arthritis, Sjorgen's syndrome, vasculitis, diseases involving leukocyte diapedesis, central nervous system inflammatory disorder, multiple organ injury syndrome secondary to septicaemia or trauma, alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex mediated diseases, inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis,
                                                                                                                                         20 EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT
                                                                                                                                                                                                                                                                                                              PPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVHN
                                                                                                                                                     VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTC
                                                                                                                                                                                                                                                                        AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                                                                                                                                                                                                QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                   84.9%; Score 2175.5; DB 19; Length 452;
88.7%; Pred. No. 5.1e-128;
iive 17; Mismatches 24; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pucabenc; human immunodeficiency virus; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                 412 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYYQKSLSLSPGK 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain of 3D6 anti-HIV antibody
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/label= Framework_1
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/label= signal
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/label= CDR-1
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/label= CDR_2
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                                                                                                               Best Local Similarity 88.7
Matches 409; Conservative
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/label= F
                                                                                  452 AA;
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                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                         15; Gaps
                                                                                                                       The variable region of the heavy chain is used in a recombinant protein with the variable region from the kappa light chain of 3D6, the two V regions being joined by a linker. The recombinant protein behinds to HIV gp160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YISHCRGGVCY--GGY----FEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                                                                                                                                                                                                                                         61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                                                 DB 13; Length 475;
Recombinant protein which binds to complex viral antigen and HIV-1 - contains variable region of antibody derived from 3D6 cell line, used for detecting HIV-1 antigen
                                                                                                                                                                                                                                                                                          84.8%; Score 2172.5; DB 13; Lengt:
86.2%; Pred. No. 8.3e-128;
ive 18; Mismatches 34; Indels
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17; Gaps

180

223

283

475

ð g RESULT 12

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61 GKGLELVAQINSV--GNSTYYPDTVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCASG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 DPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 343
                                                                                                                 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                                                                                                                                                  119 ------DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 163
                                                                                                                                                                                                                                                                         FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSSLGTQTYICNVNHKPSNT 240
                                                                                                                                                                                                                                                                                                                                                      KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
                                                                                                                                                                                                                                                                                                                                                                                                                               DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 APIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPEN 403
                                                          1 MGWSLILLFLVAVATRVOCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 461
                                                                                                                                                                                                                                                                                                                                                                          164 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                                                                                                                                                                            121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50..54 /note= "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101..110
/note= "Complementarity determining region 3"
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31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen, CDR, complementarity determining region, autoimmune diseases; rheumatoid arthritis; allergy
15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR22757 standard; Protein; 470 AA.
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  Matches 415; Conservative
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/note= "m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, beta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/per-clinical Alzheimer's disease, bown's syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266.
                                                                                                                                                                                                                                                                                                             Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanised antibody for the treatment of Alzheimer's comprises the inhibition and reduction of the formation of amyloid plaques {\color{black} -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20..461
/label= Mature_Hu266_heavy_chain
/note= "This sequence is specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2169.5; DB 22;
Pred. No. 1.2e-127;
                                                                                                                                                                                                                                                                         Humanised monoclonal antibody Hu266, heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bales KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                     AAU07745 standard; Protein; 461 AA
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86.8%;
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08-DEC-2000; 2000US-0254465.
08-DEC-2000; 2000US-0254498.
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                                                                                                                                                                                                                                  04-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 17"
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                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
Homo sapiens.
Synthetic.
                SPGK 478
                                                      472 SPGK 475
                                                                                                                                                                                                                                                                                                                                                      gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vasquez M;
                                                                                                                                                                                            AAU07745
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graft rejection;

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Query Match
Best Local Similarity 89.8
Matches 412; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPEVKPNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
                                                                                                                                                                                                                                                                                                                                                                            61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                                                                                                                                                                                                                                                                                                                                    61 GRGLEWIGFIRDKAKGYTTEYNPSVKGRVTMLVDTSKNOFSLRLSSVTAADTAVYYCARE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 APIEKTISKAKGÓPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPEN 412
                                                                                                                               The sequence is that of the reshaped CAMPATH-1 heavy chain antibody. Reshaped CD4 antibody can be used to induce tolerance against an antigen. It can also be used to alleviate autoimmune diseases such as rheumatoid arthritis, and to prevent graft rejection. Tolerance to a graft, e.g. an organ graft or a bone marrow transplantation can also be useful to alleviate allergies. Tolerance to alleview allergies Tolerance to allergens could also be achieved. See also AMR22754-R22763.
                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMFEALHNHYTQKSLSLSFGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; Hashimoto's thyroiditis; diabetes; uvetits; dermatitis; psoriasis; urticaria; nephrotic syndrome; glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                      1 MGWSCIILFLVATATGVHSQVQLEESGPGLVRPSQTLSLTCTVSGFTFTDFYMNWVRQPP
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                                                                                                                                                                                                                                                                                                                        1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                                  Humanisation of antibodies binding to human CD4 antigen - by mutation of framework-encoding regions of DNA encoding variable domain of rat or mouse antibody chain
                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                   84.4%; Score 2162; DB 13; Length 470; 86.0%; Pred. No. 3.7e-127; ive 18; Mismatches 41; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised anti-CD23 MAb C11 heavy chain.
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                                                                                                        Disclosure, Fig 5; 74pp; English.
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                                                                                                                                                                                                                                                                                              Matches 411; Conservative
             1992-132139/16
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                            470 AA;
                         N-PSDB; AAQ23570
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Best Local
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This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCERII) monoclonal antibody Cl1, composed of a human framework (HSIGKVII) and the heavy chain complementarity determining regions (see AAY3257-59) of murine antibody Cl1. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the Cl1 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on capable of binding to the CD23 type II molecule expressed on capable of binding to the CD23 type II molecule expressed on content on in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, cliabetes, uveitis, dermatitis, psoriasis, uritcaria, nephrotic syndrome, glomerulonephitis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergice asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor specific antibodies useful for treating e.g. arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eczema, graft-versus-host disease, COPD, insulitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and
inflammatory bowel disease; ulcerative colitis; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shearin J;
                               Sjogren's syndrome; allergy; asthma; rhinitis; eczema; graft-versus-host disease; COPD; bronchitis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellis JH, Rapson NT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                            "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes, multiple sclerosis and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "framework region
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                                                                                                                                                                                                                                                                     Socation/Qualifiers
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/note= "framework
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/note= "CDR 3"
                                                                                                                                                                                                                                                                                                                                                                                                               "CDR 1"
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                                                                                                  B-cell malignancy; therapy.
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                                                                                                                                                                                                                                                                                                                                            'note=
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                                                                                                                                                                                                         Synthetic.
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Gapa

Score 2161.5; DB 21; Length 444; Pred. No. 3.7e-127; 7; Mismatches 25; Indels 15;

84.4%;

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TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTCPP 225
                                                                                                                                                                                                                                                                    CPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 285
                                                                                                                                                                                                                                                                                                                                               345
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                                                                                TFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKABPKSCDKTHTCPP 259
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                                                                                                                           QGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199
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                   1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSGYWMS#VRQAPGKGLE#VAEIRLKSDNYAT
EVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWVGFIRNKPNGGTT
                                                               EYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYISHCRGGVCYGGYFEFWG
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Human recombinant immunoglobulin (Ig) heavy chain region. Z AAE12715 standard; Protein; 451 (first entry) 04-JAN-2002 AAE12715 RESULT 15 

Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; heavy chain region; cancer; breast; ovary; lung; bladder; cytostatic; therapy; immunoglobulin; Ig.

Homo sapiens

WO200175110-A2.

11-OCT-2001

30-MAR-2001; 2001WO-US10589,

30-MAR-2000; 2000US-0538913

(DYAX-) DYAX CORP

Hoogenboom HRJM, Henderikx MPG,

WPI; 2001-626437/72. N-PSDB; AAD20745.

Novel isolated tumor-associated antigen mucin-1-specific binding member for diagnosing and treating cancer, comprises mucin-1 binding domain or its portion for binding to an epitope of the protein core of mucin-1

Claim 12; Page 106-108; 126pp; English

The invention relates to an isolated tumour-associated antigen mucin-1 (MUC-1)-specific binding member comprising an antigen binding domain

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cc region having an antibody variable light (VL) or heavy (VH) region,

or a complementarity determining region (CDR) of VL or VH. MUCI-specific

CD binding member is useful for diagnosing cancer, preferably adenocarcinoma

CT he binding of MUCI-specific binding member to MUCI is detected by a

detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imagnay, solintillation counting, and X-ray film.

CMUCI-specific binding member is useful for treating cancer, preferably

adenocarcinoma, in an individual, where the cancer is present in tissue

CC the breast, ovary, lung, or bladder of the individual. MUCI-specific

CD binding member is useful for diagnosing and imaging MUCI-sepressing

cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUCI or MUCI epitope-

CC containing molecules, and for therapeutically or prophylactically

CT treating cancer. The present sequence is human recombinant immunoglobulin

CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
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                                                                                                                                                                                                                                                                                                                                                      Length 451;
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                                                                                                                                                                                                                                                                                                                                                  84.3%; Score 2160; DB 22;
89.8%; Pred. No. 4.7e-127;
iive 12; Mismatches 27;
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Matches 412; Conservative
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                                                                                                                                                                                                                                                                                                                 451 AA;
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Q8wu38 homo sapien Q96kx8 homo sapien

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Run on:

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Q9brv0 homo sapien
Q9brv0 homo sapien
Q9bqbB homo sapien
Q96dkO homo sapien
Q96dkV homo sapien
Q96wy4 homo sapien
Q96wy4 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 85.1%; Score 2178.5; DB 4; Length 471; Best Local Similarity 87.2%; Pred. No. 7.1e-181; Matches 416; Conservative 15; Mismatches 27; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A.
IISSUB-SPLEEN;
Strausberg R.;
Strausberg R.;
Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
Hypothetical protein.
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.8 kDa protein.
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11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                            90; Indels
                                                                                                                                                                                                                                                                                         Strausberg R.;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024405; AAH24405.1; -.
Hypothetical protein.
SEQUENCE 469 AA; 51976 WW; 534793F155D05457 CRC64;
                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          63.7%; Score 1632.5; DB 1:
63.0%; Pred. No. 2.1e-133;
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                                                                                                   469
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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 303; Conservative
                                                                                                 PRELIMINARY;
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01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
1810060009Rik protein.
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Best Local Similarity
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                                                                                               Q8R3V9
Q8R3V9;
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Q8R3V9
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   234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 RGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 ----VMGFGAHWGGGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 AEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                               478
                                                                                                                                                                                                                                             415 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSESPGK 471
   PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
                               PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
                                                                                                                                                               PIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENN
                                                                                                                                                                                               355 PIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LLLVAAPRWVLSRLQLQESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQPPGKGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 TISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 TISKAKGOPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                              422 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473;
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al Similarity 75.5%; Pred. No. 2.9e-151;
357; Conservative 33; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025985; AAH25985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      il protein.
473 AA; 51986 MW; E29920B09BA369F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
Homo sapiens (Human).
BUKarypota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
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Matches
 175
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SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                                                                                 Hypothetical 51.9 kDa protein. AU044919.
                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                       475 SPGK 478
                                                                                                                                                  SLGK 473
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SEQUENCE 47
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                                                                                               STRAIN-C57BL/60; TISSUE=PANCREAS;

MEDLINE=2108560; PubMed=11217851;

MEDLINE=2108560; PubMed=11217851;

Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Redischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynchaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havanhizaki V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVDKKAEPK-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
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                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.4%; Score 1495.5; DB 11; Length 473; Best Local Similarity 57.4%; Pred. No. 1.7e-121; Matches 278; Conservative 79; Mismatches 110; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OWN 1.
9DED57A514475FBB CRC64;
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INTERPO; IPR003599; IG.
INTERPO; IPR003599; IG.
INTERPO; IPR003500; IG-like.
INTERPO; IPR003006; IG-like.
INTERPO; IPR003596; IG-v.
Ffam. PF00047; IG; 4.
SWART; SW00400; IG; 2.
SWART; SW00400; IG; 3.
SWART; SW00410; IG like; 1.
PROSITE; PS00290; IG MK; 9DED5
SEQUENCE 473 AA; 51699 MW; 9DED5
                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
EMBL; AKO07918; BAB25349.1; -.
HSSP; P01842; 7FAB.
         1810060009RIK.
                                                               NCBI_TaxID=10090;
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                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 SHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPVIVSWNSGALISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNVNHKPSNTKV 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWVGFIRNKPNGGTTE--YAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTSYI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LNLVFLVLILKGVQCEVQLVESGGGLVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LILLFLVAVATRVQCEVQLVESGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGP 64
                                                                                                             350 NNRALPSPIEKTISKPRGPVRAPQVYVLPPPAEEMTKKEFSLTCMITGFLPAEIAVDWTS
                                                                              NGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 DKKAEPKSCDKT-HTCPP----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKKLEPSGPISTINPCPPCKECHKCPAPNLEGGBSVFIFPPNIKDVLMISLTPKVTCVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.8%; Score 1480.5; DB 11; Length 473; Best Local Similarity 59.2%; Pred. No. 3.5e-120; Matches 286; Conservative 69; Mismatches 105; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOLD37; AAH10327.1;
MGD; MGI:2144967; AU044319.
InterPro; IPR001045; CytC heme_bind.
InterPro; IPR001045; Ig_MHC.
Pfan, PF00197; ig; 3.
PROSITE; PS00190; CYTCCHROME C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein.
473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Q91205,
Q91205,
Q91205,
Q91205,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416
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61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
409 ELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
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                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YISHCRGGVCYGG----YFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 PSNTKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.5%; Score 1472.5; DB 11; Length 473; Best Local Similarity 57.6%; Pred. No. 1.7e-119; Matches 279; Conservative 74; Mismatches 114; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.,
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RESP: PO1042; FPRO 1989: 1; -.
RICEPPRO; PRO03599; IG.
INTERPRO; PRO03509; IG.
INTERPRO; PRO03006; Ig.—IK.
RICEPPRO; PRO03006; Ig.—IK.
RICEPPRO; PRO0407; IG. 2.
RICEPPRO; PRO0407; IG. 3.
RICEPPRO; PRO0407; IG. 3.
RICEPPRO; PRO0407; IG. 2.
RICEPPRO; PRO0409; IG. 2.
RICEPPRO; PRO0409; IG. 2.
RICEPPRO; PRO0409; IG. 1.
RICEPPRO; PRO0409; IG. 1.
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                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to RIKEN CDNA 1810060009 gene.

Mus musculus (Mouse).
                                                                                                                                         Q99L25 PRELIMINARY; PRT; Q99L25; 17: Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                     RESULT 7
Q99L25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 LPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 418
  411 GHTEENYKDTABVLDSDGSYFIXSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRS 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKCŚWVIFFLMAVVIGVNSEVÓLQQSGAELVRPGAŚVKLSCTASGFNIKDSLMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 KVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazaa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N [1]
N [1]
N SEQUENCE FROM N.A.
A Straubberg R.;
L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC003878; AAH03878.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR0035609; Ig.
DR InterPro; IPR0035600; Ig_like.
DR InterPro; IPR0035600; Ig_like.
DR InterPro; IPR003560; Ig_WHC.
DR SWART; SM00409; IG; 2.
DR SWART; SM00409; IG; 2.
DR SWART; SM00400; IG_Like; 1.
DR SWART; SM00400; IG_Like; 1.
DR SWART; SM00400; IG_Like; 1.
DR SWART; SM00400; IG_Like; 1.
DR SWART; SM00400; IG_Like; 1.
DR SWART; SM00400; IG_Like; 1.
                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to RIKEN CONA 1810060009 gene. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                        468 AA
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01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
Matches 280; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                           PGK 478
                                                                                                                                                    PGK 473
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                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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59.8%; Pred. No. 2.8e-119;
tive 68; Mismatches 92;
                                                                437 AA
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SMART; SM00406; IGv; 1.
SMART; SM00410; IG like; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
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InterPro; IPR003600; Ig like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_V.
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                                                                PRELIMINARY;
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RESULT 8
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.,

Strausberg R.,

Strausberg R.,

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

RMBL, BC003435, AAH03435.1; -.

HSSP, PO1842, TRAB.

RMD; MGI:96446, Igh-4.

R InterPro: IPR003599, Ig-1.

R InterPro: IPR0035006, Ig-1.

R InterPro: IPR003506, Ig-1.

R InterPro: IPR003506, Ig-1.

R InterPro: IPR003506, Ig-1.

R SMART; SM00407, IG-1.

R SMART; SM00407, IG-1.

R SMART; SM00407, IG-1, 2.

R SMART; SM00407, IG-1, 2.

R SMART; SM00400, IG-1, 1.

R SMART; SM00400, IG-1, IG-1, 1.

R PROSITE; PS00290, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, IG-1, 
                            OSPICA:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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SEQUENCE FROM N.A.
MEDLINE=21477448; PubMed=11593034;
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 SNGHTEENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTIS 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GKGLEWIG--RIFPGDGDTHYSGKFQGKAKLTADKSSVTAFLQLTSLTSEDSAVYFCARD 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Gaps
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                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 FPESVTVTWNSGSLSSSVHTFPALLQ-SGLYTWSSSVTVPSSTWPSQTVTCSVAHPASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
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Mammalia; Eutyeria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.3%; Score 1415; DB 11; Length 474; Best Local Similarity 55.9%; Pred. No. 1.7e-114; Matches 271; Conservative 73; Mismatches 123; Indels 18;
                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC025447; AAH25447.1; -.
Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
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                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.7 kDa protein.
                                                                    474 AA
                                                                      PRT;
                                                                      PRELIMINARY;
                                                                                                                                                                                                               Mus musculus (Mouse).
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                                                                    OBR3H6
               RESULT 10
QBR3H6
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AC 09600
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DT 01-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gabs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
49.5%; Score 1268; DB 4; Length 701;
Best Local Similarity 82.7%; Pred. No. 1.8e-101;
Matches 244; Conservative 4; Mismatches 29; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77826 MW; 94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region
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82; Mismatches 179; Indels 119;
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InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; ig; 5.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 4.
SMART; SM00406; IGV; 1.
                         Conservative
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                         Matches 208;
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                                                                                                    MEDLINE-9838416; PubMed=9717671;
Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Magner B., Overesch G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
Lorganization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
Immunobiology 199:105-119(1998).
EMBL: AJ300675; CAC44624-1;
InterPro; IPR003066; Ig_MHC.
PÉm: PF00047; ig; 2.
PROSITE; PS000290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 GLYSLSSVVIVPSSSLGTQTYICNVNHKPSNTKVDKKAEP-----KSCDKTHTCPPCPA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLDSDGSFFLYSK 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK 299
                                                                                                                                                                                                                                                                                                                                                                                                                          9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                         49.3%; Score 1262.5; DB 6; Length 337; 69.2%; Pred. No. 1.9e-101; ive 42; Mismatches 53; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.3%; Score 879.5; DB 4; Length 597; 35.4%; Pred. No. 8.7e-68;
                                                Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strauberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE S97 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                              NON_TER 1 _1 = SEQÜENCE 337 AA; 37438 MW; AGOBFZB01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
101-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 65.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 LSVDRNRWQQGTTFTCGVMHEALHNHYTQKNVSKNPGK 337
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                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 69.2%
Matches 234; Conservative
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SEQUENCE FROM N.A. Wagner B.;
                                                                                       SEQUENCE FROM N.A.
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Best Local Similarity
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TISSUE=B-CELL;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
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**096BB9** 

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18;
                                                                                                        61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                                                                                                                                                                                                      178 KDYFPEPVTVSW --NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICN 232
                                                                                                                                      61 GKGLEWYSAISG--SGGSTYYADSVKGRFTISRDNSRDTLYLOMNSLRAEDTAVYYCA-- 116
                                                                                                                                                                                      121 YISHCRGGVCYGGYF--EFWGQGALVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLV 177
                                                                                                                                                                                                                 233 VNHKPSN------TKVDKKAEPKS------CDKTHTCP----- 258
                                                                                                                                                                                                                                                                                                                                                                                       234 VQHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 ------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 REGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 ASSMCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAV 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-R 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 KTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALH 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD-- 430
Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                                                                   1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   259 -------PCPAPELLGGPS---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotheitcal 67.3 kpa protein.
Homo sapiens (Human).
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                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 FLPDSITFSWKYKNNSDISSTRGFPSVLR-GGKYAATSQVLLPSKOVMGTDEHVVCKVQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270
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Query Match 33.0%; Score 845; DB 4; Length 613;
Best Local Similarity 34.5%; Pred. No. 9e-65;
Matches 201; Conservative 84; Mismatches 178; Indels 120; Gaps
                                                                                                                                                                                                                        61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                                                                                                                                                                                                                                                                121 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKD 179
                                                                                                                                                                                                                                                                                                                                                                                 119 WSE----GV---ETFDIWGGGTMYTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 HPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICOATGFSPRQIQVSWLRE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL,PAPIEKTISKAKGQP-REP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 QVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SD 432
                                                                                                                                                1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        180 YPPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14473 fis, clone MAMMAL001080, highly similar to Homo sapiens SNC73 protein (SNC73) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 475
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                                                                                              Length 494;
                                                                                    Query Match
31,4%; Score 805; DB 4; Length 49.
Best Local Similarity 40.3%; Pred. No. 2e-61;
Matches 199; Conservative 68; Mismatches 179; Indels
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 494 AA; 53088 MW; 9AID7AEB5AEE4C0E CRC64;
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463 LAFTQKTIDRLAGK 476
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Eukaryota, Metazoa, Primates; Catarrhini; Hominidae, Homo.

1 (bases 1 to 1020)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MCC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procurement: Lou Staudt

CONA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCN2094 row: h column: 21

High quality sequence start: 21

High quality sequence start: 21

High quality sequence stop: 681.
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           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Richard for money at a column: 16
High quality sequence start: 3
High quality sequence store: 675.
Location/Qualifiers
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11 HMGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                               1273 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTTACAGCAGCTCACCGTGGAC 1332
                                                                                                                                                                                 1333 AAGAGCAGGTGGCAGCAGCAGCGCAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1392
756 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGNAGAACTACTACTAGACC 815
                                                                                           816 ACGCCTCNCGTGCACCTGCACGCTCCTTCTTCCTCTACAGCAAGCTCACGTGGGA 875
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/clone="IMAGE:6278583"
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                                                                               /clone="INAGE:5524420"
/clone lib="NIH MGC 99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
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                               organism="Homo sapiens"
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BQ706140.1 GI:21845039
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 958)
NIH-MGC http://mgc.nci.nih.gov/.
Nitional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
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              AATCTTGTGACAAAACTCACACATGCCCACCGTGCCCCAGCACCTGAACTCCTGGGGGGAC
                                                          CGTCAGTCTTCCTCTTCCCCCCAAAACCCAAAGACACCCTCATGATCTCCCGGACCCCTG
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 01
High quality sequence stop: 705.
Location/Qualifiers
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Matches 865; Conservative
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/db_xref="taxon:9606"
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/clone="INAGE:84852076"
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/clone="type="primary B-cells from tonsils (cell line)"
/lab host="NIH MGG 48"
/lab host="Drible (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoR1; colnA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5 adaptor: GGCACGAGG(0: size-selected >Sobbp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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602711498F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 926)
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                                                                                                                                                  1344 GCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 1403
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MgC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov o column: 21
High quality sequence stop: 888.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                     671 CGCCGTGGAGTGGGAGCAATGGGCAGCCGGAGAACAACAACAAGACCACGCCCCCCGT
 CGCCGTGGAGTGGGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT
                                                                           GCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG
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Contact: Robert Strausberg, Ph.D.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Nath-Moc http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                        122 CTGCAACGTGAATCACAAGCCCAGCAACACCACAAGGGGGACAAGAAAGTTGAGCCCAAATC 181
CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGGCACCCAGACCTACAT 121
                                                                                                                                                                                          750 TIGIGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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                                                            9 CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAAGCCCAAATC
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Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://ingellll.gov
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High quality sequence stop: 716.
Location/Qualifiers
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Matches 908; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.

1 (bases 1 to 901)

1 (bases 1 to 901)

2 NIH-MGC http://goc.nci.nih.gov/.

3 NIH-MGC http://goc.nci.nih.gov/.

3 Unpublished (1999)

4 Unpublished (1999)

5 Email: cgapbs-r@mail.nih.gov

7 Tissue Procuement: Dr. Mark Watson

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/organism="Homo sapiens"
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IE (bases 1 to 1029)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Lou Staudt

CONR Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLCM2095 row: g column: 10

High quality sequence stop: 723.

High quality sequence stop: 723.

I. 1025

/organism="Homo sapiens" /db\_xref="taxon:9606" /clone="IMAGE:5924769"

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                    13 ATTACTGGGGCCAGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
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                                                                    CTTCCCCCTGGCACCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT
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/clone_lib="NHF MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="bype="lymphoma, cell line"
/lab_host="bype="lymphoma, cell line"
/lab_host="bype="lymphoma, cell line"
/note="organ: lymph, vector: porns; site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GCGACGAG(G). Size-selected >500bp for average insert size
1: 8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Strateagene) and Superscript
II RT (Life Technologies). Note: this is a NH_MGC
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MENA linear EST 02-APR-2002 MENA linear EST 02-APR-2002 SY, mRNA sequence.

3Q063185.1 GI:19890681

Homo sapiens uman.

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 7 BQ063185

ACCESSION

Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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180 643 240

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763

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480 943 540

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PU/11255 887 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
5', mRNA Sequence.
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                                                                        404 TCGAATTCTGGGGCCCAGGGCGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCAT 463
                           2; Gaps
                                                                                                     1 TIGACCGCTGGGGCCAGGAAAGCTGGTCACCGTCTCAGCCTCCACCAAGGCCCAT 60
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  95.5%; Pred. No. 1.2e-191;
tive 0; Mismatches 39;
  Best Local Similarity 95.5%
Matches 868; Conservative
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/lab host="NHHOB (phage-resistant)"
/lab host="NHHOB (phage-resistant)"
/lab host="Orden splen" vector: poTB7; Site_1: XhoI; Site_2: EORI; CDNA made by oligo-dT priming. Directionally cloned into EoRIXAhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH MGC Library.

8 a 316 c 245 g 147 t 2 others
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AGENCOURT 8353641 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279643
5', mRNA sequence.
BQ708022
BQ708022.1 GI:21846921
EST.
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1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: i column: 20
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                                                                                                                                                                              604 CGAGAAAACCATCTCCAAAGCCAAAGGCCAGGCCCCGAGAACCACAGGTGTACACCTGCC 663
484 GGAGGAGCAGTACAACAGCACGTACCGTGTCAGCGTCCTCACCGTCCTGCACCAGGA 543
                                            1029 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAACAAGCCCTCCCAGCCCCCAT
                                                                        544 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCTT
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/clone="IMAGE:6279643"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

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Eukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 995)

NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Concact: Robert Strausberg, Ph.D.

Email: cgapber-r@mial.inih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linn at:

http://image.llni.gov

Plate: LLCM2002 row: 1 column: 16

High quality Sequence Stop: 718.

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                                                                                                                                                     GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC
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NIH MGC Library."
1 285 c 237 g
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Matches 810; Conservative
    mRNA sequence.
                                                                            Homo sapiens
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AGENCOURT_8347186 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6279096
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                                                                                                                  400 TACTICGAATICTGGGGCCCAGGCGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGC 459
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                                                                                                                                  7 TACTTTGACGATTGGGGCCAGGGAACGCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGG 66
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                                                          Score 819; DB 14; Length 99
Pred. No. 1.9e-190;
0; Mismatches 30; Indels
                 165 t
            259 g
NIH_MGC Library."
                                                          Query Match
Best Local Similarity 96.4%;
Matches 859; Conservative
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/clone lib="NIH MGC li3"
/lab hOst="DH10B (phage-resistant)"
/lab hOst="DH10B (phage-resistant)"
/lab hOst="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTBT; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found though the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2468 row: c column: 01
High quality sequence stop: 721.
High quality sequence stop: 721.
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                                                                      1 (bases 1 to 881)
NIH-MGC http://mgc.nci.nih.gov/.
National Insistutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:6279096"
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                                                                                                                                                                                                                                                                                                                                              1031 bp mRNA linear EST 02-APR-2002
5', mRNA sequence.
BQ064886
EG064886.1 GI:19893932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Context: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Low Staudt
Tissue Procurement: Low Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I:M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I:M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2107 row: e column: 24
High quality sequence stop: 573.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Butheria, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1031)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                         1277
1038 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCCATCGAGAAAAC 1097
                                                                                           1338 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 1397
                                               CATCTCCAAAGCCAAAGGCCAGGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 1157
                                                                                                                                                                9
              421 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCCATCGAGAAAAA 480
                                                                                                                                                                                                                                                 661 TCCCGTGCTGGACTCCGACGGCTCCTTCCTTCCTACAGCAAGCTCACCGTGGACAAGAG 720
                                                           481 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG
                                                                                                                  1218 CGACATCGCCGTGGAGTGGGAGAATGGGCAGCCGGAGACAACTACAAGACCACGCC
                                                                                                                                                              601 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC
                                                                                                                                                                                                                                                                                 1398 CTACACGCAGAAGACCCTCTCCCTGTCTCCGG 1429
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/clone="IMAGE:5929343"
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                                             1098
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AUTHORS
TITLE
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936 bp mRNA linear EST 16-JUL-2002 AGENCOURT 8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961 5', mRNA sequence.
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                                                               Gaps
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us-09-758-173-7.rst

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940 bp mRNA linear EST 16-JUL-2002
S', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 940)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                    1079 CAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT 1138
                                                                                                                                                                                                                                                                                                  TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAATGGGCAGCCGGAGA 1258
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     610 ACAACTACNAGAACACCGCCTCCCGTGGACTCCGACGGCTCCTTCTTCTTCTACTACAGC 729
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                                                                                                                                                                                            610 TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 936)
                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Counce distribution: MGC clone distribution information counce therp://image.llnl.gov
Plate: LLCWB2518 rows k column: 18
High quality sequence stop: 547.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                          BQ711727.1 GI:21850626
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/organism="Homo sapiens"
/db xref="Laxan:866"
/clone=InAcGE:6277538"
/clone=InBAGE:6277538"
/clone=InDest=10=VNH WGC 113"
/lab host="NHIOB (phage-resistant)"
/lab host="NHIOB (phage-resistant)"
/lab host="NHIOB (phage-resistant)"
/note="Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2: CoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library.

27 a _331 c _264 g 154 t 1 others
              L Ubases 1 CO 3/10.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Upubblished (1999)

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/Libral at:

http://mage.llnl.gov

Plate: LLCM2464 row: b column: 03

High quality sequence stop: 749.
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54.8%; Score 787.4; DB 14; Length 977;

Best Local Similarity 92.5%; Pred. No. 1.1e-182;

Matches 886; Conservative 0; Mismatches 57; Indels 15;
    (bases 1 to 977)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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    Length 940;
  55.4%; Score 796; DB 14; Length 94
99.3%; Pred. No. 8.4e-185;
ive 0; Mismatches 5; Indels
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        539 CACCAGGATGACTGGCTGAACGGCAAGGGTACAAGTGCAAGGTTTCCAACAAGGCCTCCCA 598
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DNA sequence of a
Primatised anti-hu
Bicistronic chimer
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Anti-HIV-1 recombi
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cDNA of the heavy
Human cDNA encodin
                                                                                                      5, 2003, 18:12:24 ; Search time 394.366 Seconds (without alignments) 8205.894 Million cell updates/sec
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Encodes heavy chai	Jasmid	-70				Plasmid Glambda-1A	Human cDNA encodin	CDNA seguence #571	Plasmid Hul9AHcncd	Human anti-HBs hea	chiT84.12 H3 heavy	Synthetic EST-deri		Human cDNA encodin	cDNA seguence #303	Human recombinant	Sequence of the ch	cDNA encoding a ra	Human cDNA encodin	Human cDNA encodin		Colon adenocarcino	Lung cancer relate	Lung cancer relate	Antibody D heavy c	Monoclonal antibod	Monoclonal antibod	Baculovirus expres	Reshaped CAMPATH-1	Plasmid pTRABac/9F	Nucleotide semienc	Vector conta. TCAE	Traget nlasmid Mol	oding a	រ ប្អ
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82.3	82.3	81.5	81.5	81.4	81.4	81.2	81.1	80.9	80.6	80.4	80.4	80.3	79.8	79.5	79.5	79.4	79.3	79.2	79.2	79.2	78.9	78.9	78.9	78.9	78.8	78.6	78.6	78.6	78.5	78.5	78.4	78.3	78.3	78.1	78.0
m	1182.2	1171.4	1171.4	1169.8	1169.4	1166.2	1165.4	1163	1158.4	1155.8	1155.4	1153.4	1147.2	1142.8	1142.8	1141.4	1139.4	1138.6	1138.6	1138.6	1133.4	1133.4	1133.4	1133.4	1131.8	1130.2	1130.2	1129.2	1127.8	1127.6	1127	1125.8	$^{\circ}$	ζ.	1121
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## ALIGNMENTS

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DE Macaque primatized 7B6 heavy chain DNA.

DE Macaque primatized 7B6 heavy chain DNA.

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Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; XW

T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; XW

T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; XW

T cell/B cell interaction; ss.

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Macaca fascicularis.

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Brams P, Hanna N;

WPI; 1998-286601/25. P-PSDB; AAW63763 Anderson DR, 

New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B for treating assesses .... \_\_\_ cells, e.g. graft rejection or tumours

This sequence encodes a primatized form of the antibody 7B6 heavy chain from macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new match antibodies (MAD be) that bind selectively to B7.1 (CD86) on to B7.2 (CD86) antiquens and inhibite binding of these antiques to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocycopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the NAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuperessants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and suriantigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression and antigen-specific immunosuppression and Example 7; Fig 4b; 87pp; English

Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;

ö 120 180 240 240 300 360 420 420 480 480 540 GIGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 120 TGTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA 180 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC 300 TATCTGCAAATGAGCAGCCTGAAAATCGAGGACACGGCCGTCTATTACTGTACTACATCC 360 Gaps 9 1 ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG 60 1 ATGGGTTGGAGCCTCATCTTGCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG TATCTGCAAATGAGCAGCCTGAAAATCGAGGACACGGCCGTCTATTACTGTACTACATCC TACATTTCACATTCTGGGGTGGTGTCTGCTATGGAGGTTACTTCGAATTCTGGGCCAG CCCTCCTCCAAGAGCACCTCTGGGGGCACAGGGGCCCTGGGCTGCTGGTCAAGGACTAC 61. GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAGAGTCTCC 121 rerecaercresarreacerreasisaceaeracarerregarreseces TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCTCAGAGATGATTCCAAAAGCATCGCC TACATTTCACATTGTCGGGGTGGTGTCTGCTATGGAGGTTACTTCGAATTCTGGGGCCAG GGCGCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA GGCGCCTGGTCACCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCA ö Score 1437; DB 19; Length 1437; Pred. No. 1.3e-277; Indels ö 0; Mismatches 100.08; Query Match Best Local Similarity 100. Matches 1437; Conservative 61 241 301 361 181 181 241 301 361 421 421 481 ઠે 셤 ે 유 ઠે g ð g ò 요 ò 요 ò g ઠે Ω ò

Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;

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1020 1020 1080 1080 1140 1200 1081 GCCCCCATCGAGAAAACCATCTCCAAAGCCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC 1140 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC 1260 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGCCTCCTTCTTCCTCTACAGAGAG 1320 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380 CTCACCGTGGACAAGAGCAGGTGGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380 099 99 720 780 840 840 900 900 960 960 720 780 DNA sequence of a primatised form of the heavy chain of 7B6 antibody. GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437 1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1437 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC <u> AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG</u> TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCCTGACCAGCGGCGTGCACACC TCCAGCAGCTTGGGCCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACC Accercargarereceggaceergaggreatargegregregregregregregregregag GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGCAACAACAGCACGTACCGTGTGGTCAGCGTCCTCTCTG TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCGAGCAACACC **AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC** ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCA caccassacrescrearescaassacracaasrecaassacrecaasaasecerecea AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTACAGCAAG AAS17245 standard; DNA; 1437 BP (first entry) AAS17245; 601 661 721 721 781 841 901 901 196 961 1021 1021 1081 1141 1141 1201 1261 1261 1321 1321 1381 541 601 781 841 661 1201 AAS17245 셤 엄 g g g g a ò d g ద qq ò ð ò ð 셤 ò à ò ò ð ð ò ò 엄 **%%8%8%8**  m

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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7.4 cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or crejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's calways disease, and other types of allergies. The present nucleic acid sequence encodes the heavy chain of T86, a primatised antibody cused in the invention to induce apoptosis.
neuroprocective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                            /*tag= a
/product= "Heavy chain of 7B6 antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;
                                                                                                                                                                                     Location/Qualifiers
1..1437
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                                                                           interleukin-2; IL-2; mutant; ds.
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                                                                                                            Chimeric - Homo sapiens.
Chimeric - Macaca sp.
Synthetic.
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                   181 GGGAAGGGCCGGAATGGGTAGGTTTCATTAGAAACAAACCGAACGGTGGGACAACAGAA
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TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC
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              1261 AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320
                                               CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
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                                                                                               1381 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1437
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                                                                                                                                                                                                                                                             Primatised anti-human B7.1 antigen antibody 786 heavy chain DNA.
                                                                                                                                                                                                                                                                                   Monoclonal antibody; cynomolgus monkey; macaque; 7B6; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopsenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type I diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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                                                                                                                                                     61 GTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGAGTCTCC
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Query Match 99.9%; Score 1435.4; DB 18; Length 1437; Best Local Similarity 99.9%; Pred. No. 2.6e-277; Matches 1436; Conservative 0; Mismatches 1; Indels 0; C

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                                                                                                            1260
                                                                                                                                                                                CTCACCGTGGACAAAAGAGCAGGTGGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
                                                                                                                                                                                                                                           CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of bicistronic chimeric idiotype plasmid VR1623, which includes the cytomegalovirus immediate-early promoter, enhancer and 5' untranablated sequences, driving the expression of mouse chimeric immunoglobulin light and heavy chain coding sequences. The transcriptional terminator region includes polyA and termination signals from the bovine growth hormone gene. The plasmid expresses a functional chimeric idiotype immunoglobulin that stimulates a partially protective B and T cell response to that stimulates a partially protective B and T cell response to AAF30313) encoding a secreted form (see AAB20187) of mouse Fms-like tyroshne kinase (Flt-3 lighand), demonstrated the ability of the present invention to enhance protection from tumour challenge in a
                                                                                                                                                                                                                                                                                        1201 AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAACCAATGGGCAGCCGGAGAAC
                                                                                                                                            AACTACAAGACCACGCCTCCCGTGCACTCCGACGGCTCCTTCTTCCTCTACAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1623;
antibody; idiotype; vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bicistronic chimeric idiotype plasmid VR1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 92-97; 149pp; English
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Chimeric - Mus musculus.
Chimeric - Bos taurus.
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                                                                                                                                                                                                                                                                            7 TGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAGGTGCAA 66
                                                                                                                                                                                                                                                                                                                                                              67 CTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCCTGTGCA
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enduse b-cell lymphoma model. Thus, the invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo a Flt-3 ligand-encoding polymuclectide such as VR6200, and 1 or more antigen- or cytokine-encoding polymuclectides.
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                                                                                                                                                                                       Length 7521;
                                                                                                                                              Sequence 7521 BP; 1879 A; 1988 C; 1858 G; 1796 T; 0 other;
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84.8%; Score 1219; DB 22;
Best Local Similarity 91.3%; Pred. No. 4.6e-234;
Matches 1307; Conservative 0; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 3930 TICTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 3989
                         3630 GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCG 3689
                                                                                                              3690 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 3749
                                                                                                                                                                                                                                              1087 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG 1146
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                                                                                                                                                                                 3750 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCCCCCAACAACAAAGCCCTCCCAGCCCCC
                                                                   967 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG
                                                                                                                                                                                                                                                                                      3810 ATCGAGAAAACCATCTCCAAAGCCAAAAGGCCAGCCCCGAGAACCACAGGTGTACACCTG
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4110 CTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGATCCTGA 4160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequence #572 encoding novel human secreted protein.
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The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The cnownian also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production, and the cell is also useful for identifying compounds that modulate expression of the polynucleotide sequences compounds that modulate expression of the polynucleotide sequences compounds the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined minunodeficiency (SCID)), autoimmune disorders (e.g. cultiple sclerosis), blood disorders (e.g. thrombocytopeania), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).

The polynucleotide sequences of the invention are also useful in gene therapy. AAS62214-AAS62838 repersent the CDNA sequences of the therapy. AAS62214-AAS62838 repersent the CDNA sequences of the
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Pred. No. 1.6e-233;
0; Mismatches 118;
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Best Local Similarity 91.0%;
Matches 1307; Conservative
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23-MAR-1993; 93WO-US02629
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                                                                                                                                                                                                                                                                                                                     AACTACAAGACCNCGCCTCCCGTGGACTCCGACGGCTCCTTCTTCTTCTTATAGCAAG 1373
                                                                                                                                                                                                                                                                                                                                             CTCACCGTGGACAAGAGCAGGTGGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
                                                                                                                                                                                                                                                                                                                                                         CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGGTCTCCAACAAAGCCCTCCCA 1133
                 CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 840
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774 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-HIV-1 recombinant antibody 447-52D heavy chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1437
                                                                                                                                                                                                                                                                                                                                                                                            1434 GAGGCTNTGTTCAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCGGGTAAATGA 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody; HV-neutralising monoclonal antibody; immunoglobulin; AIDS; acquired immune deficiency syndrome; chimeric antibody; surface glycoprotein gp120; V3 loop; ss.
                                                               GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACA
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/note= "encodes recombinantly modified 447-52D
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58 GAGGTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EBV-transformed cell lines and mouse-human heterohybridomas producing human Mabs specific for the gg120 V3 loop of HIV-1 MN isolate were obtained. Mab 447-52D was found to recognise the tetrapeptide motif GPGR, i.e. the Principal Neutralising Determinant common to the V3 loop of different HIV isolates. A recombinant Ab was produced in which the H chain V region was derived from 447-52D and to which a signal sequence and a H chain intronic sequence are appended, fused to a fragment contg. a short intronic segment of the human gamma 1 encoding domain in its genomic form.
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                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant human antibody - with HIV neutralising activity against at least two isolates, useful for preventing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83.5%; Score 1199.2; DB 14; Length 1386; Best Local Similarity 92.1%; Pred. No. 3.5e-230; Matches 1277; Conservative 0; Mismatches 103; Indels 6;
                                                                                                                                                                                                                             Pfarr DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1386 BP; 333 A; 429 C; 377 G; 247 T; 0 other;
                                                                                                                                                                                                                         Johnson LS, Mark GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Fig 2A; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection in diagnosis, etc.
    92US-0861701.
                                                                    (MERI ) MERCK & CO INC.
(JOHN/) JOHNSON L S.
(PFAR/) PFARR D S.
                                                                                                                                                                                                                         Conley AJ, Emini EA,
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P-PSDB; AAR42162.
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                 541 GIGCACACCTTCCCGGCTGTCCTACAGTCCTCCAGGACTCTACTCCCTCAGCAGCGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC
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GTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCCTCAGCAGCGTGGTG
                                                                                                     CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
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immunomodulatory, muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
neural disorder; immune system disorder; muscular disorder;
reproductive disorder; gastrointestinal disorder; renal disorder;
infectious disease; cardiovascular disorder; ss.
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90.2%; Pred. No. 1.5e-227;
ative 9; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 652; 2104pp; English.
                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                99US-0124270.
                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US05883
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Best Local Similarity 90.2°
Matches 1296; Conservative
                                                                                                                                                                                                                                                                                                                                                        Rosen CA, Ruben SM;
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P-PSDB; AAB53463.
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                                                                                                                          Homo sapiens.
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J. Immunol. 133, 365-5573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a A;Reference number: I47158; MUID:95015845; PMID:7930579
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C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S3186
R;Filpula, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb_1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
354 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 413
                                                                                                  414 GOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
                                                                                                                                                                                        A;Status: preliminary, translated from GB/EMBL/DDBJ
A;MoLecule type: mRNA
A;MoLecule type: mRNA
A;Residues: 1-328 «KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 GLYSLSSVVTVPSSSLGTQTYICNVHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GLYSLSSMYTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP---G 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
48.9%; Score 1259; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 2.2e-67;
Matches 230; Conservative 43; Mismatches 53; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: 1gG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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submitted to the EMBL Data Library, Pebruary 1993
A.PBescription: Screeing method for protein-protein interactions of cloned gene products. A.PBescription: Screeing method for protein-protein interactions of cloned gene products. A.PBESTON: S1866
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A;Accession: A53598
A;Accession: A53598
A;Actuals: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 234-251 cKIM>
C;Gomment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 358/1; 368/1
C;Gomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kappenties: An immunoglobulin heterotetramer signal immunoglobulin heterotetramer; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology cIM>
F;125-222/Domain: immunoglobulin homology cIM>
F;281-350/Domain: immunoglobulin homology cIM>
F;281-350/Domain: immunoglobulin homology cIM>
F;187-454/Domain: immunoglobulin homology cIM>
F;187-4520,288-348,394-452/Disulfide bonds: #status predicted
F;164-220,288-348,394-452/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                      Nature 235, 786, 789, 129.

A; Reference number: A02157; MUD:80120716; PMID:6766534

A; Contents: a allele
A; Accession: A02157; MUD:80120716; PMID:6766534

A; Contents: a allele
A; Accession: A02157
A; MUD:80120716; PMID:676534

A; Residues: a allele
A; Accession: A02157
A; Mud:801816, 129-1303, 189, FP', 193-474 < VAM>
A; Residues: 138-161, 12, 163-189, FP', 193-474 < VAM>
A; Residues: 138-161, 129-1303, 1979
A; Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hee
A; Rocession: A26235; MUD:80081501; PMID:117548
A; Accession: A26235; MUD:80081501; PMID:117548
A; Residues: 138-172, P', 174-189, FP', 193-376, 'T', 378-474 < TUL>
A; Residues: 138-172, P', 174-189, FP', 193-376, 'T', 378-474 < TUL>
A; Residues: 138-172, P', 174-189, FP', 193-376, 'T', 378-474 < TUL>
A; Molecule type: MRNA
A; Residues: 138-172, P', 174-189, FP', 193-376, 'T', 378-474 < TUL>
A; Molecule type: DNA
A; Residues: A26232; MUD:80081502; PMID:117549
A; Ritle: Sequence of the cloned gene for the constant region of murine gamma2b immunoglo
A; Recension: A26232
A; Molecule type: DNA
A; Residues: A26233; MUD:80181502; PMID:101813
A; Recension: PSC 761-763, 1382
A; Molecule type: DNA
A; Residues: A26233; MUD:82173203; PMID:6803173
A; Accession: A26233; MUD:82173203; PMID:6803173
A; Accession: A26233; MUD:82173203; PMID:6803173
A; Accession: A26233; MUD:82173203; PMID:6803173
A; Accession: A26233; MUD:82173203; PMID:6803173
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A;Residues: 118-161, L', 163-189, 'FP', 193-300, 'R', 302-331,'A', 333-437,'DI', 440-474 <OLL>
A;Residues: 118-161,'L', 163-189, 'FP', 193-300,'R', 302-331,'A', 333-437,'DI', 440-474 <OLL>
A;Residues: 128-161004, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-gyposylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
R;Yamawaki-Kåtaoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contente: a allele
A;Accession: A02157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
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Matches 258; Conservative 71; Mismatches 138; Indels 16; Gaps
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C,Accession: 501321
K,Accession: 501321
Ked Waele, P.; Frys, V., van de Voorde, A.; Molemans, F.; Fiers, W.
Bur. J. Biochem. 176, 287-295, 1988
A,Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed as
A,Reference number: S01320; MUID:88329081; PMID:3138116
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C,Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                              172 BSVTVTWNSGSLSSSVHTLSQALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTV 231
                                                                                                                                                                  DKKAEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 293
                                                                                                                                                                                                                                            232 DKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVV 291
                                                                                                                                                                                                                                                                                                                                        294 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS 353
                                                                                                                                                                                                                                                                                                                                                                                           354 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 GHTEBNYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRS 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
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A;Residues: 1-475 <DE1>
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Matches 258; Conservative 79; Mismatches 131; Indels
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                                                                                                                                            C;Genetics:
A;Map position: 12
A;Map position: 12
C;Superfamilion: immunoglobulin C region; immunoglobulin homology
C;Superfamilion: immunoglobulin; pyroglutamic acid
E;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <VDA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 YVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYI-HWVKQRPGEGLEWIGWIYPGSGNTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F)360-427/Domain: immunoglobulin homology <IMM>
F)1/Modified site: pyrrolidone carboxylic acid (Gln) #status experiment
F)1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F)22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F)132/Disulfide bonds: interchain #status predicted
F)224,227,229/Disulfide bonds: interchain #status predicted
F)297/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 YNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDCTTICYGGWVDVWGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 DLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.2%; Score 1370; DB 2; Length 446 Best Local Similarity 57.0%; Pred. No. 8.8e-74; Matches 261; Conservative 66; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                            F,118-214/Domain: Cl region <CHl>F,215-230/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;231-340/Domain: C2 region <CH2> F;341-446/Domain: C3 region <CH3>
                                                            A; Molecule type: protein A; Residues: 1-446 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378
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                                                                                                                                                                                                                                                                                                      PESULT 10
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: PC4436
C;Accession: PC4436
R;Akashi, S:, Kato, K.; Torizaw, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A. Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphya.
A;Reference number: JC5810; MUID:98063277; PMID:9398605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxidase activity. It is directed again
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ن</u>
                  415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|: :| ||:| :| || || EVQXVETGGGLVRPGNSLKLSCLTSGFTFSN-YRMHWLRQPPGKRLEWIAVITVKSDNYG 59
356 RIISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN
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                                                                                                                                       423 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: PC4436
A,Molecule type: protein
A;Mesidues: 1-44 AKA
C;Comment: This catalytic antibody has peroxidase oxidase activi
C;Superfamily: immunoglobulin c region; immunoglobulin homology cimm.
F;251-320/Domain: immunoglobulin homology cimm.
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted
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122 PDCTTICYG-GW-VDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
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Best Local Similarity 56.3%
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-2a chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S63339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A;Ritle: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
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                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                          356 VRIISRIKGQAREPQVYVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDK 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGPR 121
                                                                                                                                                                                                                                                                                                                                                                                                            VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOP--ENN 419
                                                                                                                                                                                                   122 PDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 181
                                                                                                                                                                                                                                                                                                                                         242 KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 301
                                                                                                                              64 GLEWIGHIYGNG--ATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGPR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSIS-----GYYYWTWIRQTP 61
                         Gaps
                                                                             LWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 DSSHAFAYASY-DFWGPGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPE
                                                                                                                                                                                                                                                                      PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

57.7%; Score 1487; DB 2; Length 374;
Best Local Similarity 62.3%; Pred. No. 8.9e-81;
Matches 297; Conservative 24; Mismatches 38; Indels 118;
                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: S72664
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-140, C', 142-374 <KH2>
A,Cessidues: 1-140, C', 142-374 <KH2>
C,Superfamily: immunoglobulin C region; immunoglobulin homology
                       61; Mismatches 112; Indels
          61.6%; Pred. No. 6.6e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: mRNA
A; Residues: 1-374 <KHA>
A; Cross-references: EMBL:X81695
R; Khamilchi, A. B. B. Data Library, September 1994
submitted to the EMBL Data Library, September 1994
                           Matches 294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S72664
         Best Local' Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 LKWIGWIYPASGNIKKYNENFKGKATLIVDTSSSTAYMQLSSLTSEDTAVYFCARAMGATA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 362
                                 180 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
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                                                                                                                                                                                                                                                                       65 LEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGPRPDC 124
                                                                                                                                              197
                                                                                                                                                                                PEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 WFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRG 64
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                                                                                                                                                                                                                                                                                                                                             318 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA
                                                                                                                             125 TTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
                                                                                                         240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.7%; Score 1408.5; DB 2; Length
56.3%; Pred. No. 5e-76;
tive 70; Mismatches 126; Indels
G-----YGOGYRFHSWGQGTLVTVSS-----YGOGYRFHSWGQGTLVTVSS
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R,Symons, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 841-850, 1989
A,Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and A,Reference number: S06610; MUID:90097956; PMID:2513487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Bacte: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S1, Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
                                                                                                                                                                                                                                                             A Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: gjycoptotein; heterotetramer; immunoglobulin; membrane protein
P;161-225/Domain: immunoglobulin homology ciMM>
F;18/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 PGKALEWVGGI-TSGGTTYYNPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARST 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 IVRIISRIKGPAREPQVYVLAPPQEELSKSTVSLICMVISFYDDYIAVEWQRNGQPESED 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--EN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RPDCTTICYGGWUDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 470;
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                             59.6%; Score 1537; DB 2; ]
62.6%; Pred. No. 1.3e-83;
ive 60; Mismatches 109;
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Matches 299, Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
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                                                                                                                                                                                                                                                                                                  A Gene: GDB:1GHG4
A/Gene: GDB:1GHG4
A/Gene: GDB:119340; OMIM:147130
A/Cross-references: GDB:119340; OMIM:147130
A/Cross-references: B13-14632.33
A/Introns: 99/1; 111/1; 221/1
A/Introns: 99/1; 111/1; 221/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IGA and IGM, the subunits associate into Id C; Superfamily: immunoglobulin C region; immunoglobulin homology
C/Seywords duplication; glycoprotein; heterotetramer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IM1>
F/20-89-110/Region: hinge
                     A; Molecule type: DNA
A; Residues: 1-327 < ELL>
A; Residues: 1-327 < ELL>
A; Rote: the sequence was determined from the germline gene
R; Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant
A; Reference number: A90249; MUID:70207560; PMID:4192699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F)134-203/Domain: immunoglobulin homology <IM2>
F)134-203/Domain: immunoglobulin homology <IM3>
F)240-307/Domain: immunoglobulin homology <IM3>
F)144/Disulfide bonds: interchain (to light chain) #status experimental
F)27-83, 141-201,247-305/Disulfide bonds: #status predicted
F)105,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F)17/Rinding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
NyAlternate names: Ig gamma-1 chain C region (clone 8.10)
G.Species: Bos primigenius taurus (cattle)
C.Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
C.Accession: S22080; S06610; Ā31303
R.Sanders, P.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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90.6%; Pred. No. 1e-86;
.ive 12; Mismatches 1
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A;Reference number: $22080
A;Accession: $22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
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Matches 299; Conservative
                                                                                                                                                                                                  A,Accession: A90249
A,Molecule type: protein
A,Residues: 1-30,81-326 <PIN>
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  A; Accession: A90933
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A; Concences: described by the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
                                                                                                                                            A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
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C;Decies: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A990333, Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A99033; MUID:83157104; PMID:6299662
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1.6e-87;
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Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immu A;Feference annober: A90233; WIDD: 22033500; PMID: 4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Astruz 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID: 69064124; PMID: 5782707
A;Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.1%; Score 1600; D 90.9%; Pred. No. 1.6e;ive 12; Mismatches
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Best Local Similarity 90.99
Matches 300; Conservative
A, Molecule type: protein
A, Residues: 238-275 <HOF>
R, Hofmann, T.; Parr, D.M.
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Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Recession: A93906

A;Rocession: A93906

A;Residues: 1.326 *ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudemberg, H.H.
J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A22809; MUID:81007873; PMID:6774012

A;Contents: myeloma protein Til
A;Accession: A92809

A;Molecule type: protein Til
A;Accession: A92809

A;Molecule type: protein Til
A;Recession: A28809

A;Note: Trp-156 is at or near the complement-binding site
B;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J: Blochem: 57, 789-767, 1979

A;Note: Trp-156 is at or near the complement-binding site
B;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J: Blochem: 57, 789-767, 1979

A;Reference number: A90752; MUID:80001357; PMID:113060

A;Reference number: A90752; MUID:80001357; PMID:113060
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A;Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A;Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D', 195-196,'Q',198
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A;Contents: Zie.
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Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
Accession: A93906; A92809; A90752; A93132; A02148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DIPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180
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                                                                                                                                                                                               147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 ------GPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
                                                                                                                         47;
                                                  Length 377;
                                                                                                                     12; Indels
                                       63.0%; Score 1624.5; DB 2; ilarity 81.7%; Pred. No. 6.8e-89; Conservative 10; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                    207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA-----
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                                                  Query Match
Best Local Similarity
Matches 308; Conserv
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c5, u) with an IGHG4 converte
      A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
Cispecias: Homo sapiens (man)
Cispecias: Homo sapiens (man)
Cibate: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
CiAccession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic, Acids Res. 14, 1779-1789, 198, 198
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507; PMID:3081877
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
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C;Species: Homo sapiens (man)
C;Accession: A60764
R;Huck, S; Lefranc, G; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Fill: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an immunogric number: A60764; MUID:90007613; PMID:2571587
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A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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F, 20-85/Domain: immunoglobulin homology <IMM>
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Matches 308; Conservative
                                                                                                                                                                                                                                                                            A; Accession: A23511
A; Molecule type: DNA
A; Residues: 1-377 <HUC>
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
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A;Gross-references: GDB:120085; OMIM:147100
A;Gross-references: GDB:120085; OMIM:147100
A;Gross-references: GDB:120085; OMIM:147100
A;Gross-references: GDB:120081; OMIM:1471; 2247
C;Gomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap ain disulfide bonds: In some cases, such as IgA and IgM; the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin hemology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMI>-
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Rsidues: 1-96, "K. 98-197, "D', 199-238, "E', 240, "M', 242-266, "D', 268-271, "D', 273-330 <SCH
A; Note: this sequence has the Gim(3) and Glm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: A90565; MUD:71064027; PMID:4923144
A; Contents: annotation; disulfide bonds
R; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Reference number: A91667; MUID:77070267; PMID:1002129
A; Contents: annotation; disulfide bonds
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                                                                                   A; Molecule type: protein
A; Residues: 1-34, Q',36-96, K',98-115, Q',117-197, 'D',199-238,'D',240,'L',242-268,'E',
A; Residues: this sequence has the Gim('I) and Glm('I) markers
A; Note: this sequence has the Gim('N', Hischmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgGl R
A; Reference number: A91723; MUID: 33899131; PMID: 6884994
A; Contents: myeloma protein KOL; disulfide bonds
A; A; Contents: myeloma protein KOL; disulfide bonds
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F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-03,144-204,252-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
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GenCore version 5.1.4 p5\_4578 Copyright (c) 1993 - 2003 Compugen\_Ltd.

OM protein - protein search, using sw model

Run on:

March 29, 2003, 09:06:24; Search time 21.3633 Seconds (without alignments) 2141.995 Million cell updates/sec

US-09-758-173-4 2577 1 MKHLWFFLLLVAAPRWVLSQ.......MHEALHNHYTQKSLSLSPGK 476 Title: Perfect score: Sequence:

283224 segs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
Result		Query				
No.	Score	Match	Length	BB	ΠD	Description
н	1763		330	н	GHHU	gamma-1 chain
7	1626.5	63.1	377	7	A23511	gamma-3 chain
n	1624.5	n	377	7	A60764	ņ
4	ø		326	7	GZHU	gamma-2 chain
2	1586.5	61.6	327	7	G4HU	gamma-
ø	1537	59.6	470	7	S22080	heavy
7	1525	59.2	472	7	831459	gamma-
œ	1487	57.7	374	7	869339	
6	0	54.7	469	7	S37483	ø
10	1376.5		444	0	PC4436	oclonal a
11	1370		4	7	S40295	gamma-2a
12	1341	52.0	474	7	G2MS11	gamma-2b
13	1329.5		~	7	S01321	gamma-2b
14	1259	48.9	N	7	147159	gamma 2a
15	1256	48.7	255	4	S31866	gamma-1 c
16	1253	•	N	7	147160	gamma 2b cha
17	1250		Э	7	PT0207	gamma ch
18	1227	47.6	N	7	147158	gamma 1 chai
19	1226.5	•	S	П	GHRB	gamma chain C
20	1223	47.5	N	7	147161	gamma 3
21	1212.5	47.1	N	Н	G2GP	gamma-2 chain
22		44.9	0	7	C30554	heavy ch
23	1152		8	П	G3HUWI	gamma-3
24	1148	44.5	2	~	PS0017	gamma-1 chain
25	1142.5	44.3	ന	~	PS0018	gamma-2b
26	13	44.2	2	Н	GIMS	gamma-1 chain
27	ч	44.1	2	П	G3MSC	gamma-3
28	m	44.0	σ	П	GIMSM	gamma-1 chain
29	1126	43.7	σ	٦	G3MSM	Ig gamma-3 chain C

	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig gamma-1 heavy c	Ig heavy chain pre	Ig mu chain - shee	Ig Y heavy chain (	Ig mu chain precur	Ig heavy chain VHI	Ig heavy chain (DO
GZMSA	G2MSAB	G2MSAM	S00847	PS0019	806611	G2MSBM	147162	S38864	A4944	S04845	S25705	B46529	S14683	869340	869131
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1122	1119.5	1117	1114.5	1108	1088.5	1080	1062	908	903	794.5	771	727.5	719	713.5	709.5
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## ALIGNMENTS

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CTGGGGGACAGCGGCCCTGGCTGCTGAGGACTACTTCCCCGAACCGGTGACGG 553 	GTGGAACTCAGGCGCCTGACCGGCGTGCACACTTCCCGGCTGTCCTACAGT 613 	CCTCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 673	AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG 733 	GCCCAAAICTIGIGACAAAACTCACACAGCCCACGGGCCCAGGACCTGAACTCCTGG 793 	<b>6 6</b>	CCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA 913 	acgiggacggcgiggaggigcataatgccaagacaaagcgggggggggg	774 ACAACAGCACGTACCGTGTGGTCACCTCCCCCCTGCACCAGGACTGGCTGAATG 1033 	argiacaagtigcaaggictccaacaaagccticccagcccccatgagaaacca 1093 	TCTCCAAAGCCAAAGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGG 1153 	TGACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGCG 1213 	ACATCGCCGTGGAGTGGGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273 	TIGGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA 1333 	GGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393 	CACGCAGAAGAGCCTCTCCCGGTAAATGA 1431 
, ctgggggaacacagc 	TGTCGTGGAACTC             TGTCGTGGAACTC		AGACCTACATCTG	AGCCCAAATCTTG             AGCCCAAATCTTG	GGGGACCGTCAGT             GGGGACCGTCAGT	cccrgaggrcac             cccrgaggrcac	ACTGGTACGTGGA                   ACTGGTACGTGGA	ACAACAGCACGTA 	GCAAGGAGTACAA 	TCTCCAAAGCCAA              TCTCCAAAGCCAA	ATGAGCTGACCAA               ATGAGCTGACCAA	ACATCGCCGTGGP 	ccgrgcrggacrc	GGTGGCAGCAGGC 	acacgcagaaga(               acacgcagaaga(
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Search completed: April 6, 2003, 06:25:14 Job time : 69.1566 secs

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Batent No. 6413717

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: WALSH, Edward E.
APPLICANT: WEREN, Cheryl Jannen
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MCNOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: MCHODS FOR THEIR MANUFACTURE AND THERRAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                            GCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAGAAAACCA 1093
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                                                    AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAAGCAG 733
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614 CCTCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACCC 673
                                                                            671 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAG 730
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                                                                                                                                                                                                                                                                 SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,697B
FILING DATE:
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/770,057
FILING DATE:
APPLICATION NUMBER: 08/770,057
                         ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
RELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-6201
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                               STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..1428
US-09-335-6978-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ن</u>
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,697B
FILING DATE: 06-Jul-2000
CLASSIFICATION: vUnknown>
PRIOR APPLICATION NUMBER: 08/770,057
FILING DATE: 4-Unknown>
APPLICATION NUMBER: 08/770,057
FILING DATE: 4-Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEFRAM: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.5%; Score 1123.6; DB 4; Length Best Local Similarity 88.5%; Pred. No. 2.8e-265; Matches 1255; Conservative 0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..1428
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-335-697B-17
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US-09-335-697B-17

US-09-335-697B-17

Sequence 17, Application US/09335697B

Patent No. 6200804

GENERAL INFORMATION:

GENERAL INFORMATION:

MALSH, Edward E.

HEARD, Cheryl Janne

NEWMAN, Roland Anthony

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND

METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
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  ACAACAGGACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAGGGGTGAATG
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                                                                                                                                  GGGGACCGTCAGTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
                                                                                                                                                                             CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
                                                                                                                                                                                                                                                                ACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
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                                                                                         GGGGACCGTCAGTCTTCCTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA
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CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis STREET: Pt.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                791
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APPLICATION NUMBER: US 08/488,376
FILING DATE: 07.-UN1-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMONICATION INFORMATION:
TELECHAN: (703) 836-6620
ITELERAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                  LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                 1..1428
                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-770-057-17
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Sequence 17, Application US/08770057

Sequence 17, Application US/08770057

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter

APPLICANT: PAN, Li-Zhen

APPLICANT: PAN, Li-Zhen

APPLICANT: NEWART, Soulaima Salim

APPLICANT: NEWART, Soulaima Anthony

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND

TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSES: Burns, Doane, Swecker & Mathis

STREET: P.O. BOX 1404

CITY: Alexandria

STATE: Virgin:
                                                                                                                     TCTCCAAAGCCAAAGGCCAGGAGAACCACAGGTGTACACCCTGCCCCATCCCGGG 1153
                                                                                                                                                                                                                                                                                                                      ACATCGCCGTGGAGTGGGAGGAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1273
                                                                                                                                                                                                                                                                                                                                                                          CCGTGCTCGACTCCGACGGCTCCTTCTTCTTCTACAGCACACCGTGGACAAGAGCA 1333
                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 1393
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                914 ACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 973
CCCCTGAGGTCACATGCTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
                                                                                                     974 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAAGGACTGGCTGAATG
                                                                GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA
                                                                                                                                                                                                                                1091 TCTCCAAAGCCAAAGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGG
                                                                                                                                                                                                                                                                  ATGAGCTGACCAAGACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGCG
                                                                                                                                                                                                                                                                                COMPOTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLIÇATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1394 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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MEDIUM TYPE: Floppy disk
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COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                      77 CTGGTCCTGTGGTGGTGAAACCCACAGAGACCCTCAGGCTGCTGCACGGTCCTCTGGGGT 136
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Query Match 78.5%; Score 1123.6; DB 2; Length Best Local Similarity 88.5%; Pred. No. 2.8e-265; Matches 1255; Conservative 0; Mismatches 154; Indels
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314 ACGTGGACCCTGTGGACACACACACATATTACTGTGC---ACGGGTAGGACTGTATGACA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1428;
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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; LOCATION: 1..1
US-08-635-878-17
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APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, ROJIANG ANTHONY
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
CORRESPONDENCE ADDRESS:
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                                            GCAAGGAGTACAAGTGCAAAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAGAAAACCA 1090
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,878
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CITY: Alexandria
STATE: Virginia
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RECISTRATION NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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US-08-635-878-17
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Pred. No. 2.8e-265;
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Matches 1255; Conservative
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Best Local Similarity
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US-08-634-400-17
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APPLICANT: GLAMAT, Soulaima Salim
APPLICANT: GLAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: HAN, Li-Zhen
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
TITLE OF INVENTION: NEUTRALIZING HICH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF OWNERS PROUBENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTNS, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandrian
STREET: Virginia
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               1091 TCTCCAAAGCCAAAGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCATCCCGGG
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COUNTRY: United States
ZIP: 2213-1404
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/634,400
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08634400 Patent No. 5939068 GENERAL INFORMATION:
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TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: WALSH, Edward E.
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Soland Anthony
TITLE OF INVENTION: MCUTALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MCHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
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            1211 ACATCGCCGTGGAGTGGGAGGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC 1270
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,224
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Patent No. 5866125
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CLASSIFICATION: 424
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197 TAGAATGGCTTGGAAACATTTTTTCGAGTGACAAAGTC---CTTCAGTCCTTCTCGA 253
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APPLICANT: GHAMT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Soulaima Salim
APPLICANT: WALSH, Soulaima Salim
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, ROITMALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCIONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: BUTNS, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
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Pred. No. 2.8e-265;
0; Mismatches 154; Indels 9;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,223
                                                                                                                                                   ACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAATGA 1428
                                                                                                                   ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 17, Application US/08634223
; Patent No. 5840298
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LOCATION:
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APPLICANT: CHAMAT; Soulaima Salim
APPLICANT: CHAMAT; Soulaima Salim
APPLICANT: CHAMAT; Soulaima Salim
APPLICANT: PRAN, Li-Zhen
APPLICANT: WALSH; Edward E.
APPLICANT: WALSH; Edward E.
APPLICANT: WERMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTNS, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
CITY: Alexandria
STREET: P.O. BOX 1404
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALIBLE
COMPUTER: IBM FC COMPALIBLE
COMPUTER: IBM FC COMPALIBLE
COMPUTER: IBM FC COMPALIBLE
COMPUTER: IBM FC COMPALIBLE
COMPUTER: IBM FC COMPALIBLE
COMPUTER: APPLICATION NUMBER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PLOSO #1 TING NUMBER
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Pred. No. 2.8e-265;
0; Mismatches 154; Indels 9;
Sequence 17, Application US/08488376
Patent No. 5811524
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NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6201
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
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; LOCATION:
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                                                                                                              -------GTAATATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTC 402
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 CTGAACTTGAATTCTGTGACCGACGCGGACACGCCCGTCTATTACTGTGCGAGAGGCCCT 360
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             APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
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                                                                                                                                                                                                                                   ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/POCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ 1D NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 1285, Conservative
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GENERAL INFORMATION:
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Patent No. 6136310
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STREET: 699 Prince Street
CITY: Alexandria
STATE: WA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT N. PC-DOS/MS-DOS
SOFTWARE: PATENT N. PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION NUMBER: 35,030
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: TEAKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 012712-165
TELEPRAY: 703-836-620
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TELEPRAY: 704-836-620
TELEPRAY: 704-836-9318
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDESS: single
TOPOLOGY: linear
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Matches 1286; Conservative
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; LOCATION: 1..1404
US-08-523-894-11
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LOCATION: 1..1404
FEATURE:
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Pred. No. 5.9e-277;
0; Mismatches 116; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain variable and constant gamma
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/523,894
FILING DATE: 06-5EP-1995
CLASSIFICATION: 424
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                                                   ....ER: US/08/523,894
06-SEP-1995
N: 424
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEFAX: 036-836-6620
TELEFAX: 036-836-6201
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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POSITION IN GENOME:
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90.0%;
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Best Local Similarity 90.0
Matches 1288; Conservative
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LOCATION:
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NAME/KEY:
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Sequence 11, Application US/08523894

Factor No. 613510.

BERIERAL INFORMATION:

APPLICANT: Hanna, Nabil

APPLICANT: Reff, Mitchell E.

TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

TITLE OF INVENTION: Therapy

UNMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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; Sequence 7, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
    APPLICANT: Hanna, Nabil
    APPLICANT: Newman, Roland A.
    APPLICANT: Reff Mitchell E.
    TITLE OF INVENTION: Therapy
    TITLE OF INVENTION: Therapy
    NUMBER OF SEQUENCES: 59
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
    STREET: 699 Prince Street
    CITY: Alexandria
    STATE: VA.
                                                                                                                                                                                                                                                                                                         901 AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGCGGAAGAGAGCAG
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                                                                             GGGGGACCCTCAGTCTTCCTCTTCCCCCCAAACCCAAGGACACCCTCATGATCTCCCGG
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                GAGCCCAAATCTTGTGACAAAACTCACACGTGCCCACGTGCCCAGCACTGAACTCCTG
                                                                                                                                                                                  ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCCACGAAGACCCTGAGGTCAAGTTC
CAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACCAAGAAGGAGAAAAGCA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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84.6%; Score 1210.4; DB 4; Length 1418;
Best Local Similarity 92.4%; Pred. No. 1.8e-286;
Matches 1310; Conservative 0; Mismatches 96; Indels 12;
                                                                                                                                                                                                                                                                                                     NAME/KEY: mat_peptide
LOCATION: 58..141
COTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY
OTHER INFORMATION: CHAIN"
   REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMONIOLICATION INPORMATION:
TELEPHANE: 703-413-3000
TELEPAX: 703-413-220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
FEATURE:
                                                                                                                                                                                                                                                          sig_peptide
1..57
                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 1..1418
FEATURE:
                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
FEATURE:
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              906 CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
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                                                                                                                  958 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC
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US-08-793-450-7

Sequence 7, Application US/08793450

Patent No. 6312690

GENERAL INFORMATION:
APPLICANT: BDELMAN:
APPLICANT: RACGARITTE, CHRISTEL
APPLICANT: CHAABIHI, HASSAN

TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SECTIANG SYSTEM: PC-DOS/MS-DOS
COMPUTER: APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: V
COUNTRY:
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CITY: AF
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                                                                                                                                                                                              86.3%; Score 1234.8; DB 3; Length 1567; 92.9%; Pred. No. 2e-292; ive 0; Mismatches 87; Indels 15;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1567 base pairs
; TYPE: nucleic acid
; TYPE: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANCTUT01
; CLONE: 1513264
US-09-049-672A-17
                                                                                                                                                                                            Query Match
Best Local Similarity 92.99
Matches 1332; Conservative
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; Sequence 17, Application US/09049672A
; Patent No. 6135941
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TELEFAX: 650-845-4166
TELEX:
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                                                                      Length 1431;
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                                                                          Score 1315.8; DB 3; Length
Pred. No. 3.3e-312;
0; Mismatches 72; Indels
                                                                        DB 3;
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                                                                                                                      Conservative
             LOCATION: 1..1431
                                                                          Query Match
Best Local Similarity
Matches 1359; Conserv
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US-08-487-550-11
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GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCCTCCCAGCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY DAY

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
OSOFTWARE: FASTENCEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REGISTRATION NUMBER: 39,132
REGISTRATION NUMBER: 39,132
REGISTRATION NUMBER: PF-0497 US
TELEPONMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONNEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "MONNEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF ITLE OF INVENTION: IMMUNOSUPPRESANTS"

TITLE OF INVENTION: IMMUNOSUPPRESANTS"

TORRESPONDENCES 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street

CITY: Alexandria
                                                                                                                                                                                                                                                                                                                          CTGCACACACACACACACACAGAGGCCTCTCCCTGTCTCCGGGTAAATGA 1431
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
PILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECHN: 703-83-6620
TELECKX: 703-83-6201
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANBEDNESS: not relevant
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; Sequence 11, Application US/08487550
; Patent No. 6113898
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FEATURE:
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-672A-17

US-08-523-894-17

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US-08-634-224-17

US-08-634-224-17

US-08-634-400-17

US-08-634-400-17

US-08-634-17

US-09-335-697B-17

US-09-335-697B-17

US-08-634-400-19

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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                             Sequence 49,
Sequence Sequence B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 1431;
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MEDITOR TYPE: FIDOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 012712-131
TELEPHONE: 703-836-620
TELEPHONE: 703-836-620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                             US-08-457-918-8
US-08-467-420A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1431;
                                                                                                                                                                                                                                                78-08-487-550-3
; Sequence 3, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=8222190; PubMed=6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Gane segments encoding membrane domains of immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-I- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. THE MAJOR SPECIES ENCODES MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END. ENCODED IN SEGMENT OF MU CHAINS: THAT IS HOMOLOGGUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 440
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
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R HSSP, PO1842; JRAB.

R HSSP; PO1842; JRAB.

R MGD; MGI:96443; JGh-1.

R InterPro; IPR001369; Ig_MHC.

R InterPro; IPR001360; Ig_like.

R Pfam; PF00047; JG; Z.

R SMART; SM00410; IG_like; 1.

R SMART; SM0040; IG_MHC; 1.

R PROSITE; PS00299; IG_MHC; 1.

R Transmembrane; Alternative splicing.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 gamma-2A chain C region, membrane-bound form.
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                                                                                                                                                                                                                                       325 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
                                                                                                                                                                                                                                                                                          385 DELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSDGSFFLYSKLTVDKS 444
                                                                               147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
                                                                                            Gaps
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                           Length 399;
                                                     Indels
399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;
                          43.3%; Score 1117; DB 1;
ilarity 63.4%; Pred. No. 1.1e-71;
Conservative 43; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329
                                                                                                                                                                                                                                                                                                                                               445 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
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Matches 210; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| |||| || || || || || || ||| || ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 
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"Determination of the primary structure of a mouse IgG2a
immunoglobulin:amino-acid sequence of the Fc fragment. Implications
for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
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                                                                                                                                                                                                                                                                                     de Preval C., Fougereau M.; "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Biochem. 30:452-462(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 4e-72;
43; Mismatches 74; Indels
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PIR, A02152; GZMSA.
HSSP, PD1842; 7F8.
HSSP, PD1842; 7F8.
InterPro; IPR03506; Ig_MHC.
InterPro; IPR03597; Ig_C1.
InterPro; IPR03597; Ig_C1.
Fam. PF00047; ig; 2.
SWART; SW00411; IG like; 1.
SWART; SW00401; IG_Ike; 1.
PROSITE; PS00290; IG_C1, 2.
PROSITE; PS00290; IG_C1, 2.
Immunoglobulin domain; Immunoglobulin C region.
                       Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
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                                                                MYELOMA PROTEIN MOPC 173.
MEDLINE=74175517; PubMed=4831970;
                                                                                                                                                                                                                                         DISULFIDE BONDS.
MEDLINE=73056887; PubMed=4565406;
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Matches 211; Conservative
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107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-82037777; PubMed-6794027;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Williple amino acid substitutions between murine gamma 2a heavy
chain Fc regions Gigla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4011-4035(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-82037861, PubMed-6170065, Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; Multiple differences between the nucleic acid sequences of the IGG2aa and IgG2ab alleles of the mouse."; Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003500; Ig_like.
InterPro; IPR003600; Ig_like.
SWART; SW00410; Ig_like; 1.
SWART; SW00410; IG_Rike; 1.
IGMUNOSITE; PS00250; IG_MHC.
IMMUNOSIDDULIN domain; Immunoglobulin C region.
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                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1996 (Rel. 38, Last annotation update)
19 gamma-2A chain C region, B allele.
Mus musculus (Mouse).
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299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 330
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PIR; A02153; G2MSAB.
HSSP; P01842; 7FAB.
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Matches 206; Conservative
                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                      GCAB MOUSE
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GCAB_MOUSE
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GCAA MOUSE
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                                                                                                    --SSVPIFPPRKEXDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 172
                                                                                                                                                           444
                                                                                                                                                                                                                  SERVANDELICMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS 292
                            264
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                                                                                                                                            YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 384
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
  1 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD
                             207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPP--CPAPELL
                                                       -LYTLSSSVTVPSSPRPSBTVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV-
                                                                                     265 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                     DELTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig MHC.
InterPro; IPR003507; Ig cl.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.
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MEDLINE=84041483; PubMed=6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1986 (Rel. 02, Created)
01-NGC-1991 (Rel. 19, Last sequence update)
1-VUC-1999 (Rel. 18, Last annotation update)
1g gamma-3 chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                               398 AA.
                                                                                                                                                                                                                                                             RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
                                                                                                                                                                                                                                                                         293 NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 323
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EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; AQ2155; GBNSM.
HSSP; P01857; 1FC1.
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SEQUENCE FROM N.A.
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P03987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   60 FYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-1PKPSTPPGSSCPPGNILG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 QMSKKKVSLTCLVTNPFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDTDS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FKUM N.A.
MEDLINE=8119876; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene
"The complete nucleotide sequence of mouse immunoglobin gamma and evolution of heavy chain genes: further evidence for intervening and evolution of heavy chain genes: further evidence for intervening
                                                                                                                                                                                                                                                                                 148 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 207
                                                                                                                                                                                                                                                                                                                                                          208 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCP--PCPAPELLG 265
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                       43.7%; Score 1126; DB 1; Length 398; 63.8%; Pred. No. 2.6e-72;
                                                                                                                                                                                                                                               69; Indels
                                                 CH3.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
E - G (IN REF. 2).
E - O (IN REF. 2).
P -> F (IN REF. 2).
W, CF7F264B50A41B95 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                               46; Mismatches
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CH1.
HINGE.
CH2.
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                                                                                                                                                                      43929 MW;
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363
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398 AA;
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147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 GPSVFIFPPRFKDALMISLTPRVJCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 QMSKKKVSLTCLVINFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDTDS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 ELTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKSR 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00451; -; NOT_ANNOTATED_CDS.
RISSP; P01857; ITEMS.
A InterPro; IPR003006; IG_MHC.
A InterPro; IPR003507; IG_C1.
A InterPro; IPR0047; IG_1 ike.
REART; SM00410; IG_1 ike; 1.
REMRI; SM00410; IG_1 ike; 1.
REMRI; SM00407; IGG1; 2.
REMRI; SM00407; IGG1; 2.
REMRI; SM00407; IGG1; 2.
REMRI; SM00407; IGG1; 2.
REMRI; SM00407; IGG1; 3.
REMRI; SM00407; IGG1; 3.
REMRI; SM00407; IGG1; 3.
REMRI; SM00407; IGG1; 3.
REMRI; SM00407; IGG1; 3.
REMRI; SM00407; IGG1; 3.
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REMRI; SM00407; IGG1; 3.
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01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
19 gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,
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44.1%; Score 1137; DB 1; Length 329;
Best Local Similarity 64.0%; Pred. No. 3.5e-73;
Matches 212; Conservative 46; Mismatches 69; Indels
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223 CH2.
327 CH3.
36228 MW, F45827174182BAD6 CRC64;
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Cell 18:559-568(1979)
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329 AA;
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Yamawaki-Katacka Y., Nakai S., Miyata T., Honjo T.;

Yamawaki-Katacka Y., Nakai S., Miyata T., Honjo T.;

Yamawaki-Katacka Y., Nakai S., Miyata T., Honjo T.;

"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEGMENT OF MU CHAINS. THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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44.0%; Score 1133; DB 1; Length 393;

Best Local Similarity 61.9%; Pred. No. 8.3e-73;

Matches 205; Conservative 55; Mismatches 61; Indels 10; Gaps
SEQUENCE OF 121-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.
"mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
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BEDLINES BA115295; PubMed=6799207;
ROGETS J., Choi E., Souza L., Carter C., Word C.J., Kuehl | Eisenberg D., Wall R.;
Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
Cell 26:19-27(1981).
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CYTOPLASMIC (POTENTIAL).
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MGD; MGI:96446; 1Gh-4.
InterPro; 1PR003006; 1g_MHC.
InterPro; 1PR003597; 1g_C1.
SMART; SM00407; 1G; 3.
PROSITE; PS00290; 1G_MHC; 1.
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MEDLINE=80012837; PubMed=113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 76-234 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
Obata M., Yamawaki-Katacka Y., Takahashi N., Katacka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=80045036; PubMed=115593; Honjo T., Cataoka T., Kawakami T., Takahashi N., Mano Y.; Takahashi N., Mano Y.; Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene."; Cell 18:559-568(1979).
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Biochem. J. 126.837-850(1972).
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"Evolution of immunoglobulin subclasses. Primary structure of murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IRR003597; Ig_cl.
SMART; SM00407; Igcl. 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
11g gamma-1 chain C region.
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MEDLINE=73008889; PubMed=5073237;
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
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GlycoSuiteDB; P01868; -.
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16 GOCT-2001 (Rel. 40, Last annotation update)
19 gamma-3 chain C region, secreted form.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=85027161; PubMed=6092053;

Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

Tucker P.W., Blattner F.R.;

"Structural analysis of the murine IgG3 constant region gene.";

EMBO J. 3:2041-2046(1984).
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INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
INTERCHAIN (WITH A HEAVY CHAIN)
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Matches 206; Conservative
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MEDLINE=8932738; PubMed=3149946;
Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                     185 QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSD
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35946 MW; 013BAB45EF49B9DA CRC64;
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44.5%; Score 1148; DB 1; Length 326;
Best Local Similarity 63.1%; Pred. No. 5.7e-74;
Matches 210; Conservative 52; Mismatches 61; Indels 10;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G gamma-1 chain C region.
Rattus norvegicus (Rat).
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ENGUENCE FROM N.A.

MEDLINE=89232738; PubMed=3149946;

MEDLINE=89232738; PubMed=3149946;

Brueggemann M.;

Brueggemann M.;

Evolution of the rat immunoglobulin gamma heavy-chain gene family.";

Gene 74:473-482 (1988).

MENSP; PS0018; PS0018.

RISSP; PR003106; Ig MHC.

RICETPO; IPR003507; Ig_C1.

RICETPO; IPR003507; Ig_L1.

RICETPO; IPR003507; Ig_L1.

RICETPO; IRR003607; Ig_13.

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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44.3%; Score 1142.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 1.4e-73;
Matches 214; Conservative 44; Mismatches 69; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2B chain C region.
                                                                                                                                                                                                                                                                   333 AA
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat
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147
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333 AA;
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                                                                          236 RDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLTV 295
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-!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
QYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPS 235
                                              384 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 441
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MISCELLANBOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.
MISCELLANBOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
"Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin B.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Michaelsen T.E., Frangione B., Franklin B.C.;
"Primary structure of the 'hinge' region of human IgG3. Probable
quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=77021516; PubMed=823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.; "The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC)
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                                                                                                                                                DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
                                                                                                                                                                        296 DKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
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21-JUL-1986 (Rel. 01, Last seq
15-JUN-2002 (Rel. 41, Last ann
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SEQUENCE (DISEASE PROTEIN WIS)
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P01860;
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SEGMENT (12-28).

7 the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch). 251 KTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 310 184 EMBL, J00021; AAA52805.1; ALT\_SEQ.
PIR; A02149; G3HUWI.
HSSP; P01857; 1FC1.
GGGenew, HGMC:5527; IGHG3.
MIM; 147120; -.
InterPro; IPR003506; Ig\_MHC.
InterPro; IPR003500; Ig\_like.
Pfam; PF00047; ig; 2.
SMART; SM00410; IG like; 1.
SMART; SM00407; IGG1; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat. Gaps 64 DIMER). DIMER). DIMER). DIMER). 210 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKV--------DKKAEPKSCD 65 TPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDG DIMER). DIMER). DIMER). 311 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG DIMER) . DIMER). Length 290; CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN I CHAIN REMOVED POST-TRANSLATIONALLY Indels PYRROLIDONE CARBOXYLIC ACID 290 AA; 32331 MW; E69CBC95705B2F46 CRC64; INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI INTERCHAIN (WITH HEAVY CI HEAVY 44.9%; Score 1157; DB 1;  $S \rightarrow N \ (I\overline{N} \ OMM) \ .$   $/FTId=VAR \ n^{1/2}$ QV -> EB (IN ZUC). /FTId=VAR 003890. P -> L (IN OMM). /FTId=VAR\_003891. 1.1e-74; INTERCHAIN (WITH INTERCHAIN (WITH 1=VAR 003891 Y (IN OMM) FTIG=VAR 003892 -> A (IN OMM). 003895 (GLCNAC 003896  $F \rightarrow Y (\overline{IN})$  OMM) /FIId=VAR 00389 20; Mismatches F -> Y (IN Pred. No. FTIG=VAR N-LINKED 76.28; Matches 218; Conservative 279 182 227 Local Similarity 227 279 134 139 182 227 DISULFID DISULFID CARBOHYD MOD RES DOMAIN DOMAIN REPEAT REPEAT REPEAT MOD\_RES CARBOHYD DISULFID DISULFID DISULFID SEQUENCE Query Match DISULFID DISULFID DISULFID DISULFID VARIANT VARIANT /ARIANT VARIANT JARIANT VARIANT /ARIANT DOMAIN 셤 ò ò g

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Biochemistry 10:26-31(1991).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
PIR; A02151; G2GP.
                                                                                                        Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
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                                                                                                                                                                                                                                                                                                        SEQUENCE OF 227-311.
MEDLINE=75036073; PubMed=4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 SGLYSLTSMYTVPSSQKAT----CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPEN
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R InterPro; IPR003506; Ig_MHC.
InterPro; IPR003507; Ig_C1.
R InterPro; IPR003507; Ig_L2.
R InterPro; IPR003507; Ig_L3.
R InterPro; IPR003507; Ig_L3.
R InterPro; ISR00407; Ig_L3.
R SWART; SW00410; IG_L3.
R SWART; SW00401; IG_L3.
R PROSITE; PS00290; IG_MHC; 1.
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T DISULRID 16 IG_ISBURD; INTERCHAIN (WITH A LIGHT CHAIN).
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47.1%; Score 1212.5; DB 1; Length 329;
Best Local Similarity 70.1%; Pred. No. 1.6e-78;
Matches 234; Conservative 28; Mismatches 63; Indels 9;
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MEDLINE=7034672; Pubmed=4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig
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 "Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the r
half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                        WEDLINE=71058486; PubMed=5538616;
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                                                                                                                                                                                                                                                                              Biochemistry 13:4796-4803(1974).
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                                                                            SEQUENCE OF 69-133 AND 312-329
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329 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig gamma-2 chain C region.
Gavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                Query Match
47.6%; Score 1226.5; DB 1; Length 323;
Best Local Similarity 69.7%; Pred. No. 1.7e-79;
Matches 228; Conservative 34; Mismatches 58; Indels 7;
                                                                                     T -> M (IN D11 MARKER).

T -> A (IN E15 MARKER).

N -> E (IN REF. 2).

Q -> E (IN REF. 3 AND 4).

Q -> E (IN REF. 3 AND 5).

N -> D (IN REF. 5).

Q -> E (IN REF. 5).

Q -> E (IN REF. 5).

Q -> E (IN REF. 5).

D (IN REF. 5).

E -> Q (IN REF. 5).

E -> G (IN REF. 5).

N -> D (IN REF. 5).

E -> G (IN REF. 5).

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N -> D (IN REF. 5).

N -> D (IN REF. 5).
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                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Submitted (APR-1975) to the PIR data bank
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Birshtein B.K., Hussain Q.Z., Cebra J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVFSCSVMHEALHNHYTQKSLSLSPGK 476
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InterPro; IPR003597; Ig_cl.
              STANDARD;
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284
323 AA;
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P01862;
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178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
                                      387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain
                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                   323 AA
                                                                                                                                               QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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MEDLINE=76135469; PubMed=1243651;
Pratt D.M., Mole L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=83299917; PubMed=6193512;
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Biochem. J. 116:249-259(1970).
                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003006; Ig MHC
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PIR; A02161; GHRB.
HSSP; P01857; 1FC1.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      GC_RABIT
P01870;
                                                                                                                          447
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                                                                                                                                                                                                                                                                                                                           Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.; "Human immunoglobulin subclasses. Partial amino acid sequence of constant region of a gamma 4 chain."; Biochem. J. 117:33-47(1970).
                                                                               Bukaryora, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 327;
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35940 MW; 3EDBD811EF208E7A CRC64;
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    Last annotation update)
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HINGE.
CH2.
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                                                                                                                                                                                                                                                                                                                 MEDLINE=70207560; PubMed=4192699;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM0410; IG_like; 1.
SMART; SM0407; IG_like; 1.
PR0SITE; PS00290; IG_NHC; 2.
                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-30 AND 81-326
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    16-OCT-2001 (Rel. 40, Last
19 gamma-4 chain C region
IGHG4.
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Genew; HGNC:5528; IGHG4.
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327
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109
                                                                (Human)
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327 AA;
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                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                          NCBI_TaxID=9606;
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                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
gamma
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D11 AND E15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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HINGE.
CH2.
                                                                   EMBL; J00230; AAB59393.1; -. PIR; A02148; G2HU.
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                                                                                             HSSP; P01857; 1FC1.
Genew: HGNC:5526; IGHG2.
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Best Local Similarity
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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326 REMOVED POST-TRANSLATIONALLY (PROBABLE

60 S -> A (IN MYELOWA PROTEINS TIL & ZIE)

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109 C -> S (IN REF. 3).
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InterPro; IPR003500; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SW00410; Ig_like; 1.
SMART; SW00407; IG_like; 1.
SMART; SW00710; IG_like; 1.
Immunoglobulin domain; Immunoglobulin C region.
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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.
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Blochemistry 2.0:201-2270(1981).

MARKER, FTB GIM (17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKERS, 198-DEFENS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

MISCELLANBOUS: BU ALSO DIFFERS IN THE AMIDATION STATES OF 15,116,198,269 & 272.

155,166,177,195,198, 269, AND 272 AND IN THE OFBER OF RESIDUES 268-272.
                                                                                      MEDLINE=77070267; PubMed=1002129;
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SWART; SW00410; IG_like; 1.
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Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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K -> R (IN GIM(3) WARKER).
//FIG=VAR 003886.
D -> E (IN GIM(NON-1) MARKER).
//FIG=VAR 003887.
L -> M (IN GIM(NON-1) MARKER).
//FIG=VAR_003888.
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PIR; A02146; GHHU.
PDB, IFCL, 15-JUL-92.
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"The covalent structure of a human gamma G-immunoglobulin. X.
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MEDINIE-71064024; DubMed=548977;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-82274238; PubMed-6287432;
Bliston J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
Nucleic Acids Res. 10:4071-4079(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments {\rm H5-H7."}_i, Biochemistry 9:3171-3181(1970).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                P01876
P20758
P01877
P01824
P23086
P01825
P01822
P18531
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MEDIANE-71.064025; PubMed=5530842;
RULISHAUSET U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
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MEDLINE=77070269; PubMed=826475;
Ponstingl H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a
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16-OCT-2001 (Rel. 40, Last annotation update)
1g gamma-1 chain C region.
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                HVC2_HETFR
HVCM_HETFR
ALC1_HUMAN
ALC1_GORGO
ALC2_HUMAN
HV2F_HUMAN
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HV2G_HUMAN
HV46_MOUSE
HV60_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP- 372
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                                                                                                                                                                              Indels 123; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                               Length 597;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC019235, AAH19235.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003506; Ig.MHC.
InterPro; IPR003506; Ig.W.
PF00047; ig.5.
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_11ke; 1.
PROSTIE; PS00290; IG_MHC; UNKNOWN 3.
SEQUENCE 597 AA; 65300 MM; 2DĀFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 64.4 kpa protein.
                                                                                                                         36.8%; Score 948.5; DB 4;
37.7%; Pred. No. 5.1e-70;
tive 75; Mismatches 169;
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Matches 222; Conservative
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                                                                                                                                                                                                                             Query Match 36.5%; Score 940.5; DB 4; Length 588; Best Local Similarity 37.5%; Pred. No. 2.3e-69; Matches 220; Conservative 76; Mismatches 167; Indels 123; Gaps
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SMART; SM00409; IG; 2.
SWART; SM00407; IGcl; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG MHC; UNKNOWN_3.
PROSITE; PS00290; IG MHC; UNKNOWN_3.
SEQUENCE 588 AA; 64438 WW; FCGODBAD82B39FD7 CRC64;
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PRELIMINARY;
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TISSUE=LYMPH;
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                                                                                                                                                                                                                                                                                                  120 PELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTRP 179
                                                                                                                                                                                                                                                                                                                                                             240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK 299
                                                                                                                                                                                                                     GLYSLSSVVITVPSSSLGTQTYICNVNHKPSNTKVDKKAEP-----KSCDKTHTCPPCPA 260
                                                                                                                                                                                                                                                61 GPYSLSSMYTVPASTWTSETYICNVVHAASNFKVDKRIEPIPDNHQKVCDMS-KCPKCPA 119
                                                                                                                                                                                                                                                                                  PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 320
                                                                                                                                                                                                                                                                                                                                             REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 380
                                                                                                                                                                                                                                                                                                                                                                                                       381 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK 438
                                                                                                                                                        147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206
                                                                                                                                                                           1 ASTTAPKVFALAPGCGTTSDSTVALGCLVSGYFPEPVKVSWNSGSLTSGVHTFPSVLQSS 60
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.9%; Score 950.5; DB 4; Length 597; 37.7%; Pred. No. 3.5e-70; .ive 76; Mismatches 168; Indels 123;
                                                                                        49.0%; Score 1262.5; DB 6; Length 337; 69.2%; Pred. No. 2.3e-96; tive 42; Mismatches 53; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BRO03597 AAH02963.1; -.
RIACEPPO: IPR003599; Ig.
InterPro: IPR003599; Ig.
InterPro: IPR003060; Ig_like.
InterPro: IPR003060; Ig_like.
RIACEPPO: IPR003069; Ig_NHC.
RIACEPPO: IPR003069; Ig_V.
RIACEPPO: IPR003099; Ig, S.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00410; IG_like; 1.
RIACEPPO: IFS00290; IG_MHC; UNKNOWN_3.
RIACEPPO: IFS00290; IG_MHC; UNKNOWN_3.
RIACEPPO: IFS00290; IG_MHC; UNKNOWN_3.
RIACEPPO: IFS00290; IG_MHC; UNKNOWN_3.
RIACEPPO: IFS00290; IG_MHC; UNKNOWN_3.
RIACEPPO: IFS00290; IG_MHC; UNKNOWN_3.
                                                            337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l protein.
597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-070-2001 (TrEMBLrel. 17, Created)
01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 65.3 kPa protein.
Homo sepiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 AA
                Pfam, PF00047, ig, 2. ~-
PROSITE, PS00290, IG_MHC, UNKNOWN 2.
 InterPro; IPR003006; Ig_MHC
                                                                                        Query Match
Best Local Similarity 69.2%
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.7%;
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=LYMPH;
                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BU10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439
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Q9BU10
                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                261
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1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT

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410
                                          PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCAR-- 118
                                                                  60 PGKGLEWIGEINHSG-STNYNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVI 118
                                                                                                                                                                                                                   VKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-IC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 ---GPRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVPPLAPSSKSTSG-GTAALGCL 174
                                                                                                                                                                      119 TRASPGTDGR---YG--MDVWGQGTTVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCL 173
                                                                                                                                                                                                                                                        174 AQDFLPDSITFSWKYKNNSDISSTRGFPSVLR-GGKYAATSQVLLPSKDVMQGTDEHVVC 232
                                                                                                                                                                                                                                                                                                                                             233 KVOHPNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICOATGFSPROIQVSW 292
                                                                                                                                                                                                                                                                                                                                                                                                                                 293 LREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP- 372
MKHLWFFLLLLVAAPRWVLSQVQLQQWGAGLLKPSETLSLTCGVYGGSFSG-YYWSWIRQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 NVNHKPSN------TKVDKKAEPKS-------CDKTHTCP----
                                                                                                                                                                                                                                                                                                                                                                                         411 VKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 -SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BQB8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Uhknown (protein for MGC:1905) (protein for MGC:1228).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; p018825; 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 5.
SWART; SW00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R ;
Submitted (JAN-2001) to the
EMBL; BC006180; AAH06180.1;
EMBL; BC001872; AAH01872.1;
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SEQUENCE FROM N.A.
MEDLINE=99383416; PubMed=9717671;
MEDLINE=99383416; PubMed=9717671;
Magner B., Oversech G., Sheoran A., Holmes M., Richards C.,
Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS---NTKVD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 GSAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           587 EKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 VSWGQGCATVG-----HFGVY-----TRVSQYIEWLQKLMRSEPRPGVLLRAPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 EKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 49.2%; Score 1268; DB 4; Length 701; Best Local Similarity 82.7%; Pred. No. 2.2e-96; Matches 244; Conservative 4; Mismatches 29; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647 TIPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wagner B.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77826 MW; 94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
InterPro; IPR001881; EGF Ca.
InterPro; IPR001264; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF000089; Itypsin; 1.
Pfam; PF000089; Itypsin; 1.
Pfam; PF000089; Itypsin; 1.
PROSITE; PS00010; ASK HYDROXYL; UNKNOWN 1.
PROSITE; PS01086; EGF=1; UNKNOWN 1.
PROSITE; PS01187; EGF=2; UNKNOWN 1.
PROSITE; PS01187; EGF=2; UNKNOWN 1.
PROSITE; PS01187; EGF=2; UNKNOWN 1.
PROSITE; PS01240; TRYPSIN DOM; 1.
PROSITE; PS001240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; UNKNOWN 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 IGRIFPGDGDTHYSGKFQGKAXLTADKSSVTAFLQLTSLTSEDSAVYFCARDSD----- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 CYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 -YGDYFDDWGQGATVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 SCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVDVSEDDP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 IGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGPRPDCTTI 127
                                                                                                                                                                                                                                                                                                                                          51.4%; Score 1125; DB 11; Length 474;
54.0%; Pred. No. 2.5e-101;
ative 73; Mismatches 130; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLLVAAPRWYLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGXYYWTWIRQTPGRGLEW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                           Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025447; AAR125477.1; -.
Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Factor VII active site mutant immunoconjugate.
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01-DEC-2001 (TYEMBLrel. 19, Last seq
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Hypothetical 51.7 kDa protein.
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Best Local Similarity 54.0*
Matches 257; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 LEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYWTWIRQTPGRGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 FLVLIL--KGVQCEVQLVESGGGLVKPGGSRKLSCAASGFTFSD-YGMHWVRQAPEKGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 ICYGGW---VDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 AEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOP
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 IVSWNSGALISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNVNHKPSNTKVDKK
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54.0%; Pred. No. 4.9e-102;
tive 72; Mismatches 124; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC010327; AAH10327.1; -.
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InterPro; IPR000345; CytC heme_bind.
InterPro; IPR0003006; Ig_MHC.
InterPro; IPR0003006; Ig_MHC.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
BROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.9 kDa protein.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                        PRELIMINARY;
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 CARGPRPDCTTICYG---GWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALG 172
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                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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STRUMBERG R.;

L. SUDMILLEG (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC003888; AH403888.1; -..

R. HSSP; P01842; 7FAB.

R. InterPro; IPR003599; Ig.

R. InterPro; IPR003500; Ig_like.

R. InterPro; IPR003500; Ig_like.

R. InterPro; IPR003500; Ig_like.

R. InterPro; IPR003586; Ig_wHC.

R. RARRT; SM00409; IG; 2.

R. SWART; SM00409; IG; 2.

R. SWART; SM00400; IG; 1.

R. SWART; SM00410; IG; 1.

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53.7%; Score 1383.5; DB 11; Lengt;
Best Local Similarity 55.3%; Pred. No. 3.5e-106;
Matches 269; Conservative 71; Mismatches 123; Indels
                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annocation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                        PRELIMINARY;
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MGD; MGI:96446; Igh-4.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                                       PRELIMINARY;
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                                               471 LGK 473
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            Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa K., Izawa M., Nishik K., Kiyosawa H., Kondo S., Yamanaka I., Baito T., Okazaki Y., Gojobori. Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T., Pefischmann W., Gasteriand T., Gissi C., King B., Kochiwa H., A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Boffelli D., Bojinga N., Carninci P., de Bonaldo M.F., Black J., Boffelli D., Bojinga N., Carninci P., Gasukaldo M.F., A Lyons P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P., A Lyons P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P., A Lyons P., Ring B., Ringwald M., Rodriguez I., Salameto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.5%; Score 1403.5; DB 11; Length 473; 54.9%; Pred. No. 7.7e-108; ive 79; Mismatches 122; Indels 17;
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MGD; MGI:96443; 1gh-1.
INCEPTO; IPRO03599; Ig-cl.
INCEPTO; IPRO03599; Ig-cl.
INCEPTO; IPRO03006; Ig-MGC.
INCEPTO; IPRO0356; Ig-V.
FRam; PRO0479; Ig-cl.
INCEPTO; IPRO0479; Ig-cl.
SWART; SWO0409; IG-cl.
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SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Clonding of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scPV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; --
HSSP; P01842; 7FAB.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
                                            Created)
Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-UTN-2002 (TrEMBLrel. 21, Last anno
Gammal heavy chain of Mab7 (Fragment)
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SMART; SM00406; IGv; 1.
SMART; SM0410; IG like; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
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[1] -
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=PANCREAS;
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Best Local Similarity
                                                             SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 DKKIVPRDCG----CKPCICTVPEV---SSVFIFPPRFKDVLTILLTPKVTCVVVDISKD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 DPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDMLNGKEFKCRVNSAAFP 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 YYSYDLFAY-----WGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP 173
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
similar to RIKEN cDNA 1810060009 gene.
Mus musculus (Mouse).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                       Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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55.2%; Score 1423.5; DB 11; Length
Best Local Similarity 54.8%; Pred. No. 1.7e-109;
Matches 262; Conservative 84; Mismatches 115; Indels
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                                                                                                                                                                                                         SEQUENCE FROM N.A.
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118 ----nllyggyydywgggttitvssakttapsvyplapvcgdttgssytlgclvkgyfp 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 PEGGLEWIGWIDPEDGETKYAPKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCAR-- 117
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%; Score 1405; DB 11; Length 468; 56.7%; Pred. No. 5.7e-108; ive 65; Mismatches 130; Indels 12.
                                                                                     InterPro; IRR03559; Ig.
InterPro; IRR03559; Ig.
InterPro; IRR03559; Ig.
InterPro; IRR03506; Ig_like.
InterPro; IRR03006; Ig_WHC.
InterPro; IRR03596; Ig_V.
Pfam; PR00407; Ig; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00410; IG 12.
SMART; SM00410; IG Idv; 1.
SMART; PR00299; IG WHC; UNKNOWN 1.
PROSITE; PR00299; IG WHC; UNKNOWN 1.
SROUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
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Last annotation update)
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O9DBL4 01-JUN-2001 (TrEMBLE1. 17, C:
01-JUN-2001 (TrEMBLE1. 17, L:
01-DEC-2001 (TrEMBLE1. 19, L:
181006009Rik protein.
IGH-1 OR 1810060009RIK.
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099LC4 PRELIMINARY; PRT; 463 AA.
099LC4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                          55.5%; Score 1429; DB 11; 56.0%; Pred. No. 5.9e-110; tive 78; Mismatches 110;
                                                                                      Æ
                                                                                      469
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Matches 270; Conservative
                                                                                   PRELIMINARY;
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                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                  Q8R3V9
Q8R3V9;
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                                         240 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 299
                                                                           NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 364
                                                                                         300 NWYVDGVEVHNAKTKFREEQYNSTYRVVSVLTYVLHQDWLNGKEYKCKVSNKALPAPIEKT 359
                                                                                                                               ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 424
                                                                                                                                                TPGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 H-----LVMGFGAHWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||:||| VDKRVESK---YGPPCPSCFAPEFLGGPSVFLFPPKPKDTLMISKIPEVTCVVVDVSQED 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTYLHQDWLNGKEYKCKVSNKALPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 PJEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENN 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSI-SGYYYWTWIRQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Gaps
180 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV
                         EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 YKTTPPVĽDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
Hypothetical 52.0 kDa protein.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                  Query Match
78.3%; Score 2017; DB 4; Length 473;
Best Local Similarity 81.3%; Pred. No. 1.2e-158;
Matches 388; Conservative 29; Mismatches 48; Indels 1;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025985; AAH25985.1; -.
Hypothetical protein.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
                                                                                                                                                                                                                                                                             PRELIMINARY;
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TISSUE=KIDNEY;
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                          245
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RPDC----TIICYGGWVDVWGPGDLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVK 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 GYFPEPUTVTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTWPSQTVTCNVAHPAS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTKVDKKAEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LWF-FLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 469;
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                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                             Strausberg R.; Submitted (MRX-2002) to the EMBL/GenBank/DDBJ databases Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases Hypothetical protein. SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kPa protein.
Mus musculus (Mouse).
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musculu musculu sapien

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08WUKI 09C1KI 09C3A6 091X92 09CK68 09BKV0 09BKV0 091WRI 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 09UZV7 0

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Q96ey0 homo e Q96kx8 homo e Q96bb9 homo e Q99m22 mus n Q8vcx7 mus n

Q99M22 Q8VCX7

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65 LEWIGHIYGNGATINYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGPRPDC 124
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Best Local Similarity 82.8%; Pred. No. 1.1e-160;
Matches 391; Conservative 22; Mismatches 52; Indels
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Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
Hypothetical protein.
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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01-UUN-2002 (TEMBLrel. 21, Created)
01-UUN-2002 (TEMBLrel. 21, Last sequence update)
01-UUN-2002 (TEMBLrel. 21, Last annotation update)
Hypothetical 51.8 kDa protein.
Homo sapiens (Human)
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QB163 homo sapien
QB139 mus musculu
Q99131 mus musculu
Q96144 mus musculu
Q96125 mus musculu
Q91205 mus musculu
Q91266 mus musculu
Q91306 mus sapien
Q9594 homo sapien
Q9594 homo sapien
Q9504 homo sapien
Q9504 homo sapien
Q9648 homo sapien
Q9648 homo sapien
                                                                                                                                                                      March 29, 2003, 09:06:23 ; Search time 43.1716 Seconds (without alignments) 2271.829 Million cell updates/sec
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                             GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q98L25
Q91Z05
Q98C98
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sp_bacteria.*
sp_fungi.*
sp_human:*
sp_invertebrate.*
sp_mammal:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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Match 1
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the invention
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                                                                                               420
                                                                                                                            411
 DKRVESK----YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDP 291
                                                292 EVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS 351
                                                                                                                                                                                                                                                                                                                                                                                       region, CDR; single chain antibody; ScFv; infection; CD81; E2 protein; NS1 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remedies for hepatitis C containing substances with antiviral effects e.g. antibodies, proteins, sulfated polysaccharides and low-molecular compounds, by inhibiting binding of hepatitis C virus envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyamura T;
                                                                                                            301 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                          361 IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                       KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                         Matsuura Y,
                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a single chain antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 105-108; 138pp; Japanese.
                                                                                                                                                                                                                                                                AAG63640 standard; Protein; 475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MITS-) MITSUBISHI-TOKYO PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                      Complementarity determining hepatitis C virus; HCV; HCV envelope glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2001; 2001WO-JP00967
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Query Match 81.8%; Score 2107.5; DB 22; Lengtl Best Local Similarity 84.3%; Pred. No. 1.6e-118; Matches 402; Conservative 19; Mismatches 53; Indels

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 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNOFFLNLNSVTDADTAVYYCARGP 120
                                                                                             PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
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                                                                                                                                                                                         PEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
                                                                                                                                                                                                      PIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENN 419
                                                                                                                                                                                                                                                      YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475
              YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                               RPDCTT-ICYGGWUDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
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